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# HUMAN xiap

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Fig. 1 (page 1 of 7)

# HUMAN xiap

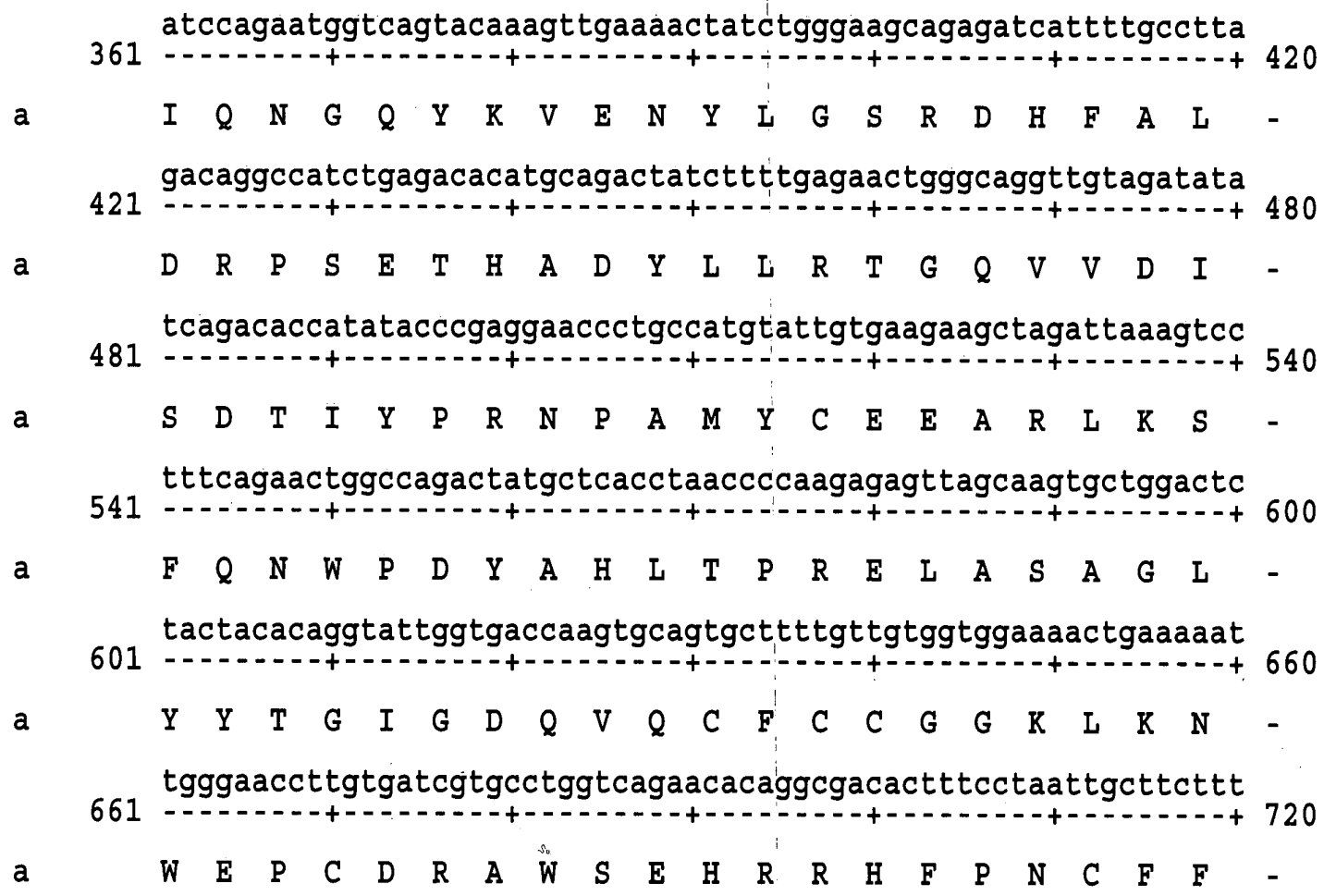


Fig. 1 (page 2 of 7)

Title: MAMMALIAN IAP GENE FAMILY, PRIMERS, PROBES ...
Applicant(s): Robert G. Korneluk et al.
Client/Matter No.: 07891/003005
Filing Date: September 1, 2000 Serial No.: 09/654,743
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HUMAN xiap

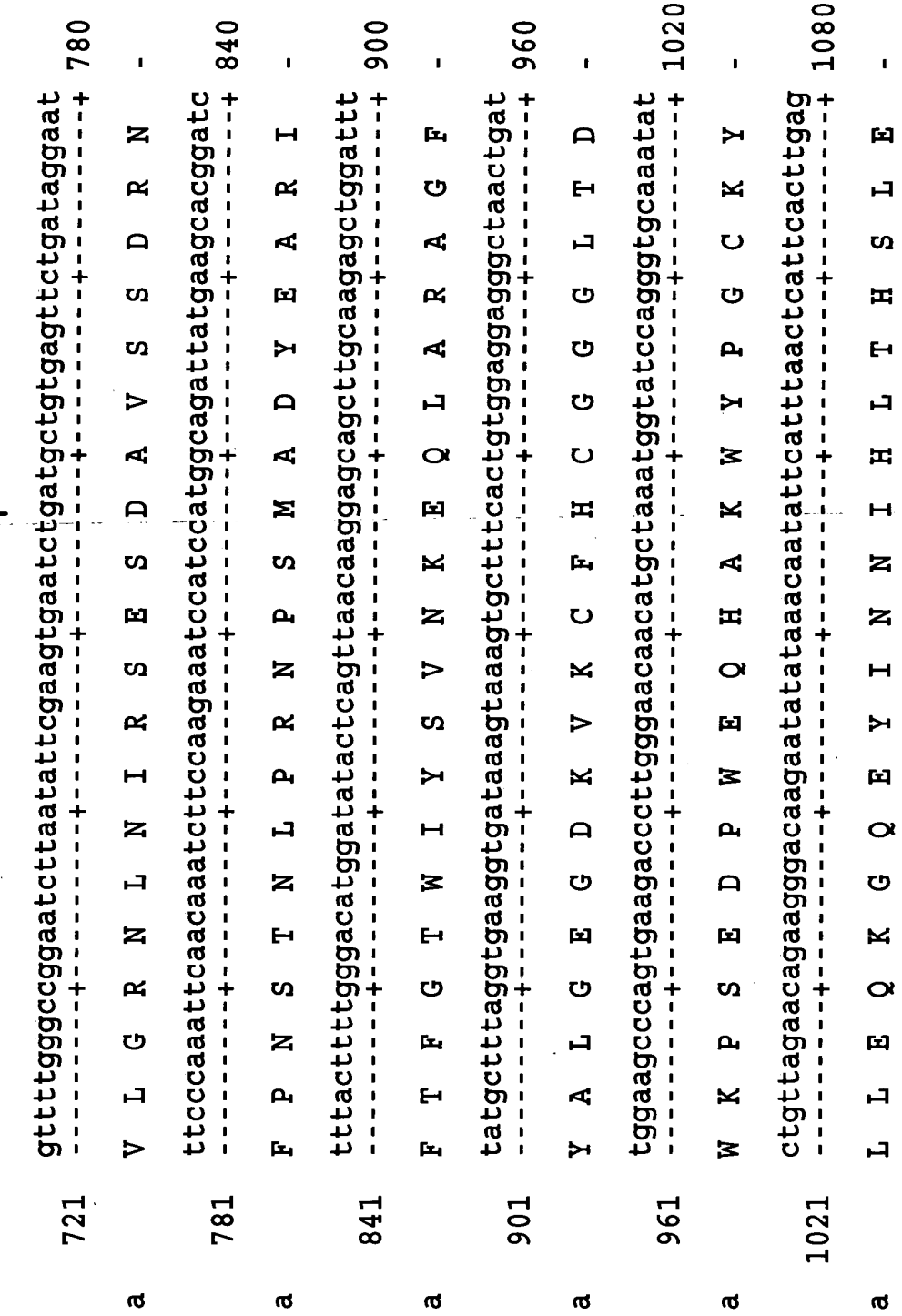


Fig. 1 (page 3 of 7)

# HUMAN xiap

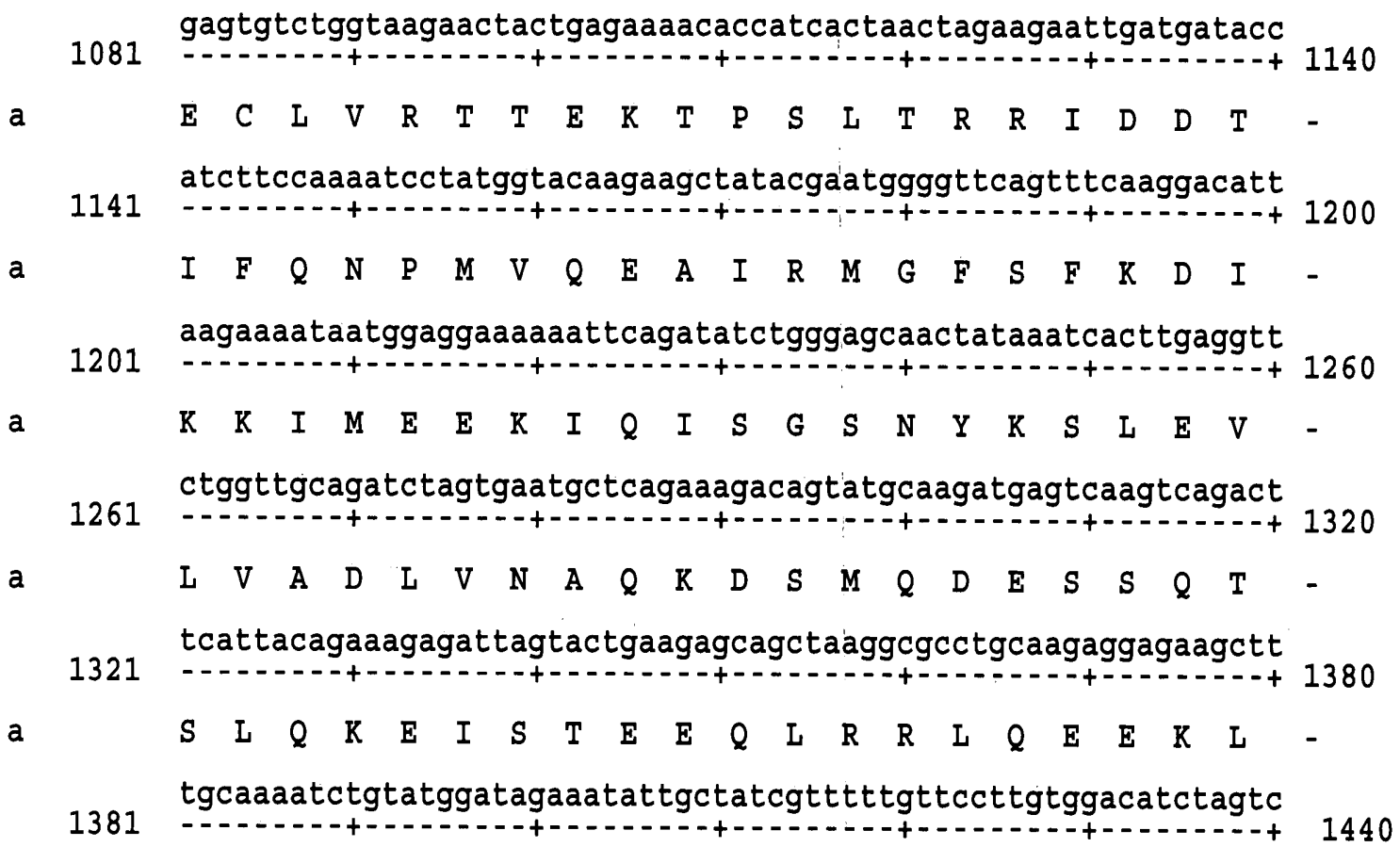


Fig. 1 (page 4 of 7)

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# HUMAN xiap

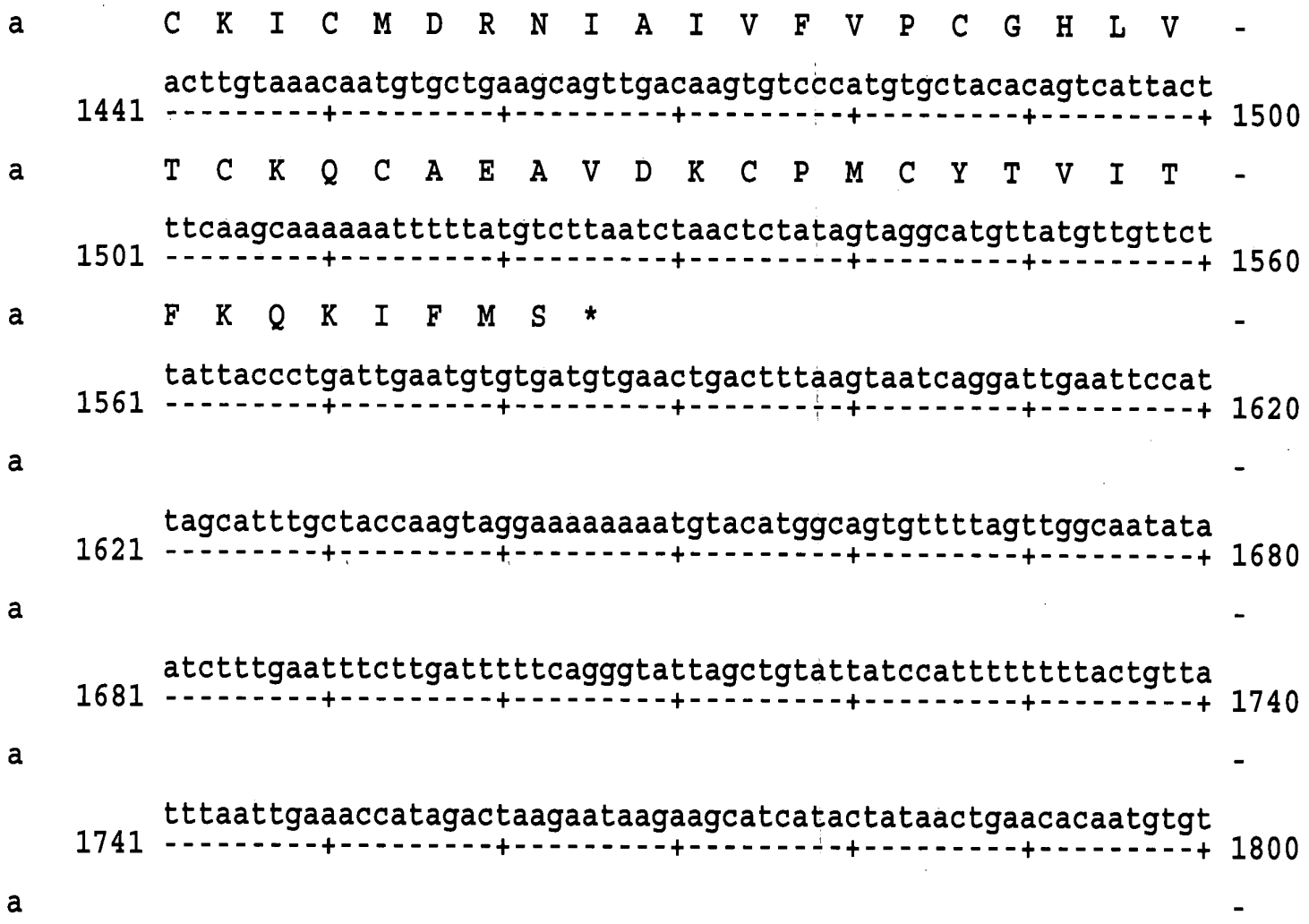


Fig. 1 (page 5 of 7)

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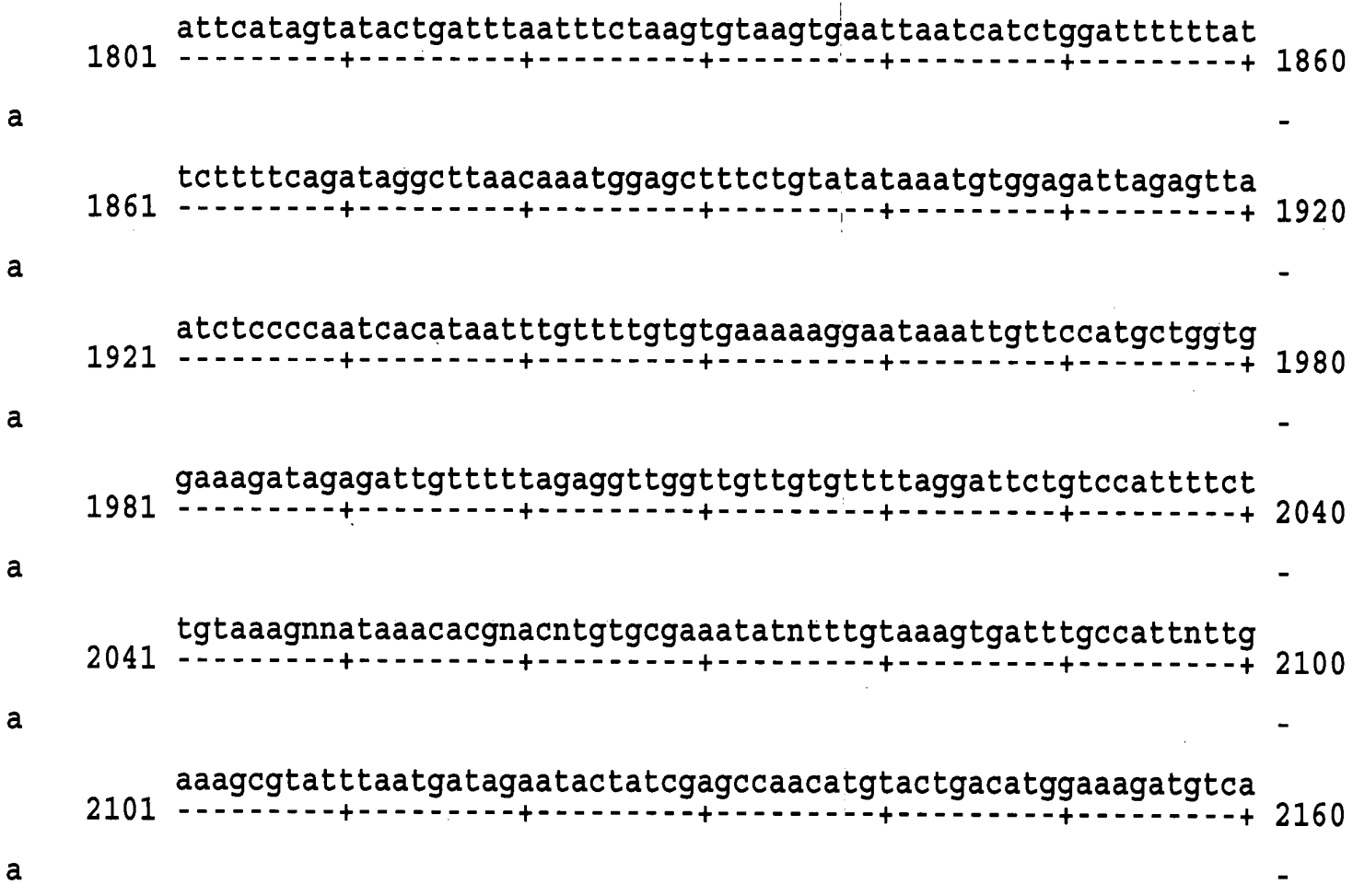


Fig. 1 (page 6 of 7)

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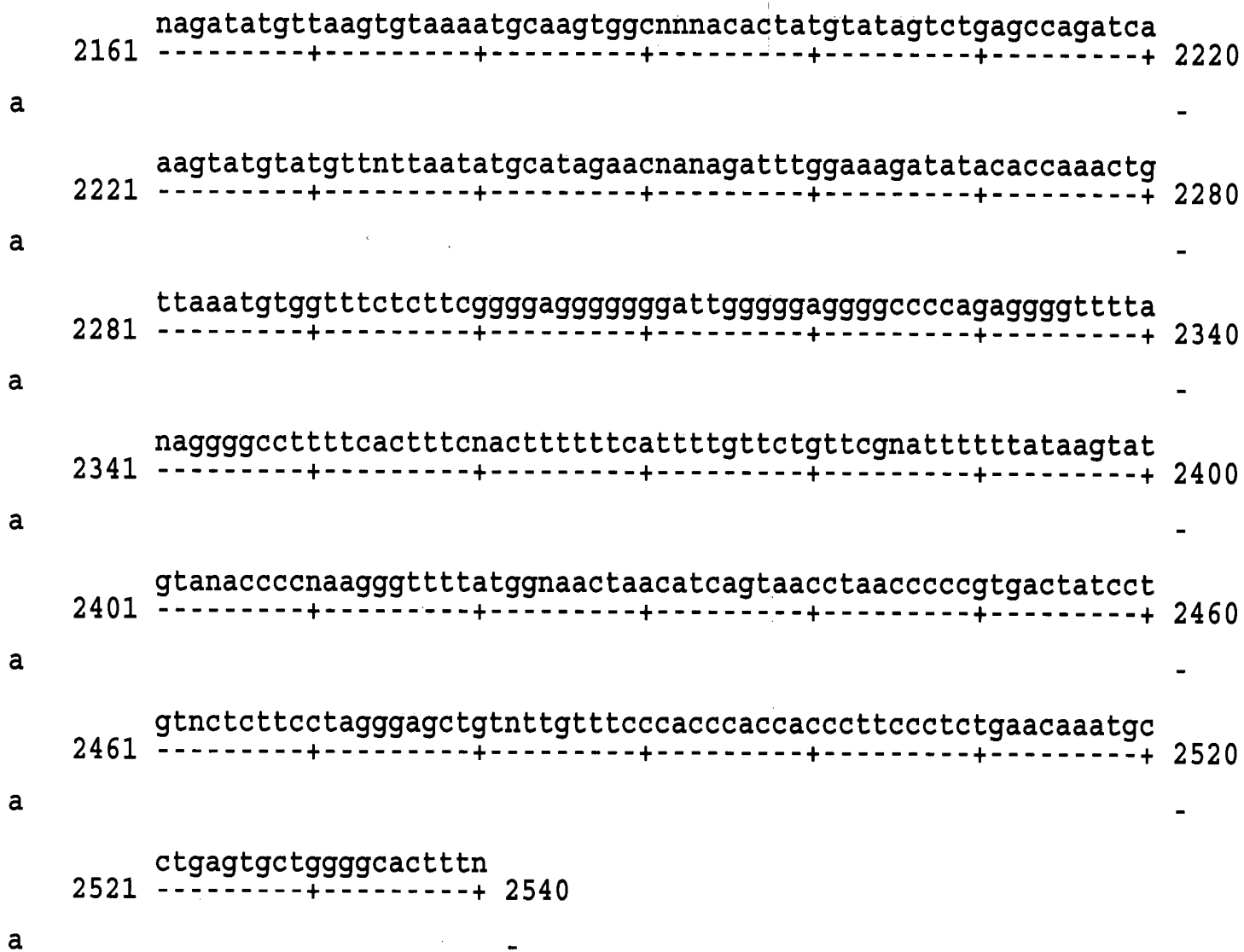


Fig. 1 (page 7 of 7)

# HUMAN hiap-1

Fig. 2 (page 1 of 8)



Title: MAMMALIAN IAP GENE FAMILY, PRIMERS, PROBES ...
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# HUMAN hiap-1

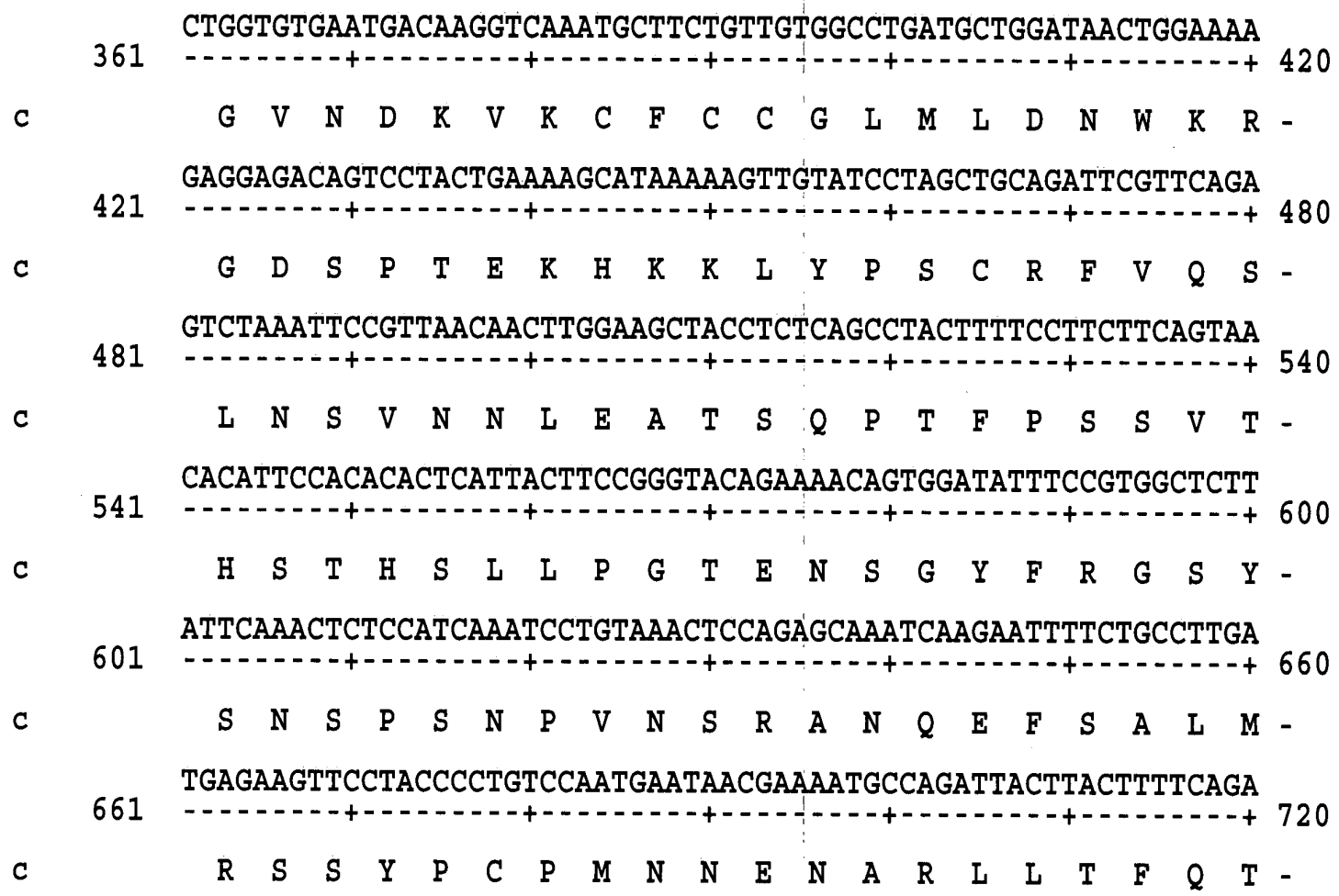


Fig. 2 (page 2 of 8)

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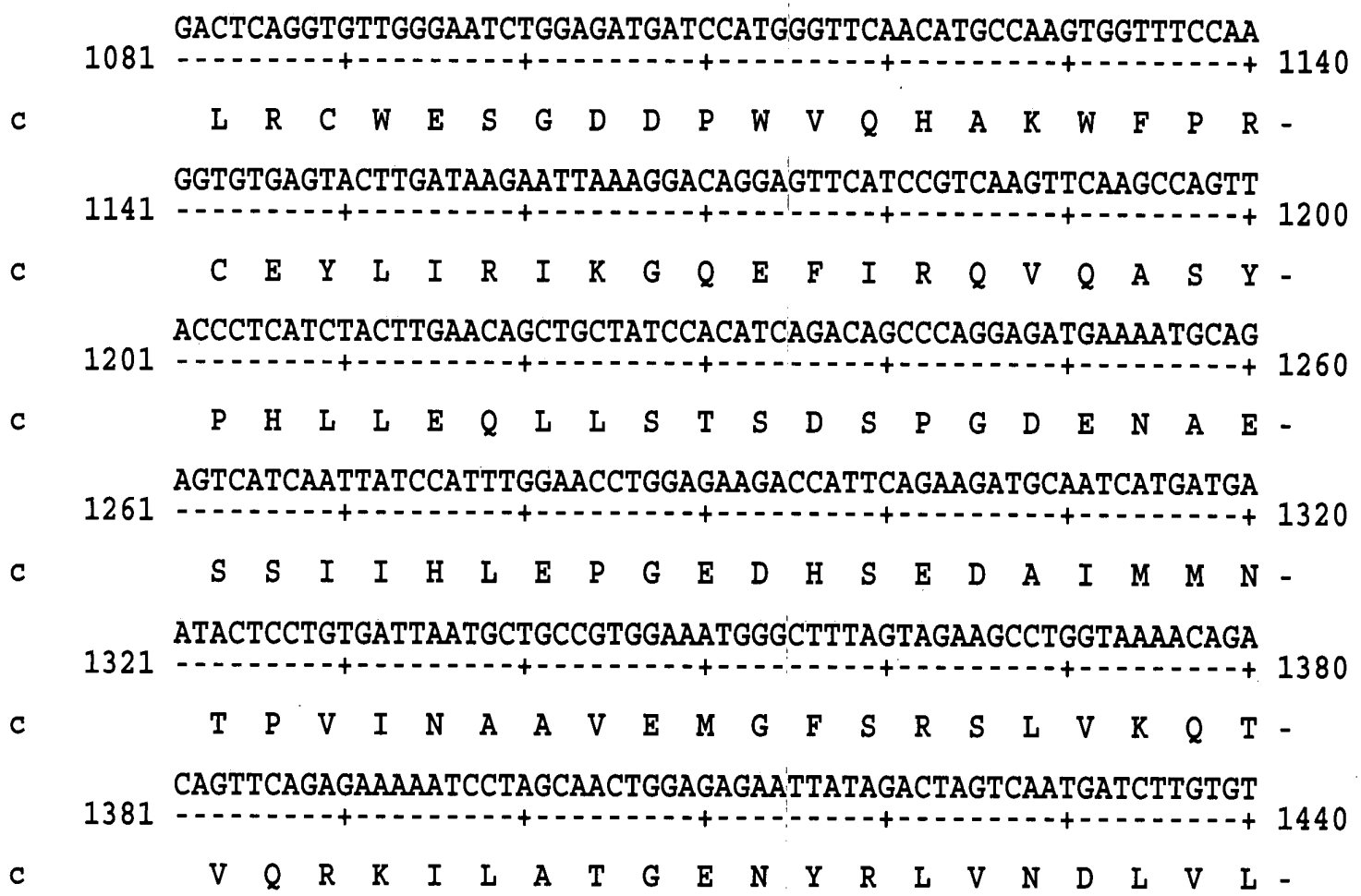


Fig. 2 (page 4 of 8)

# HUMAN hiap-1

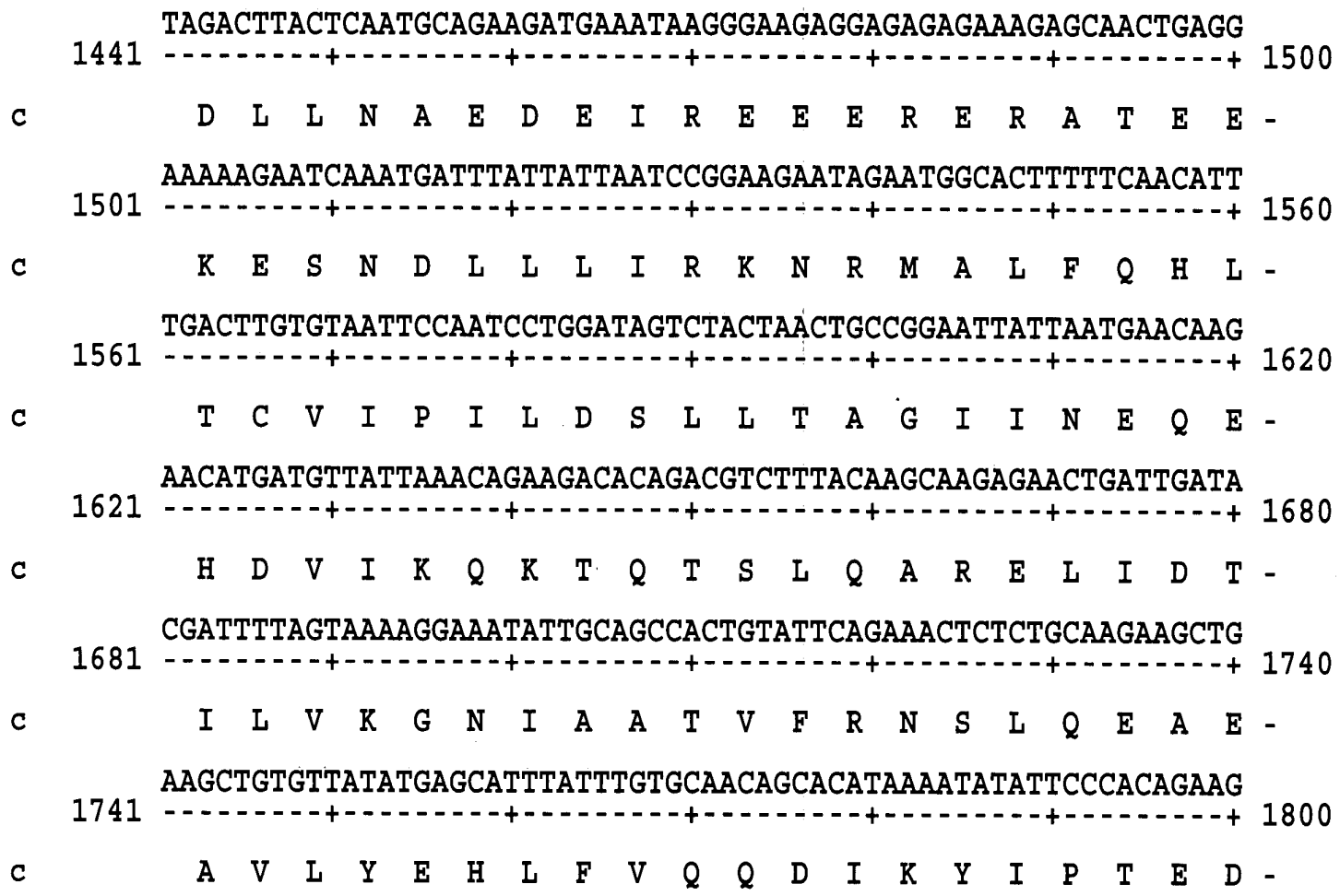


Fig. 2 (page 5 of 8)



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Client/Matter No.: 07891/003005
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# HUMAN hiap-1

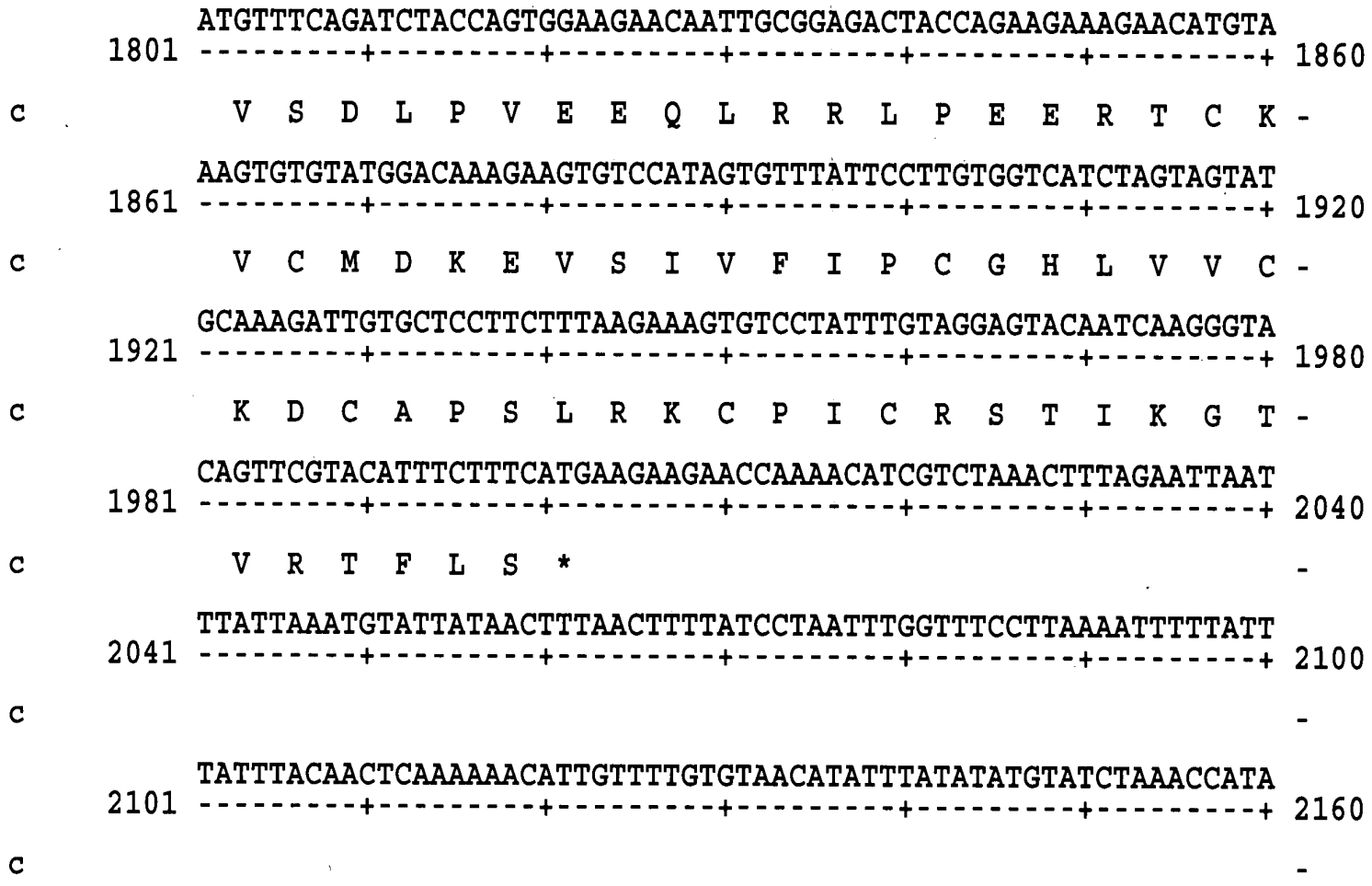


Fig. 2 (page 6 of 8)

# HUMAN hiap-1

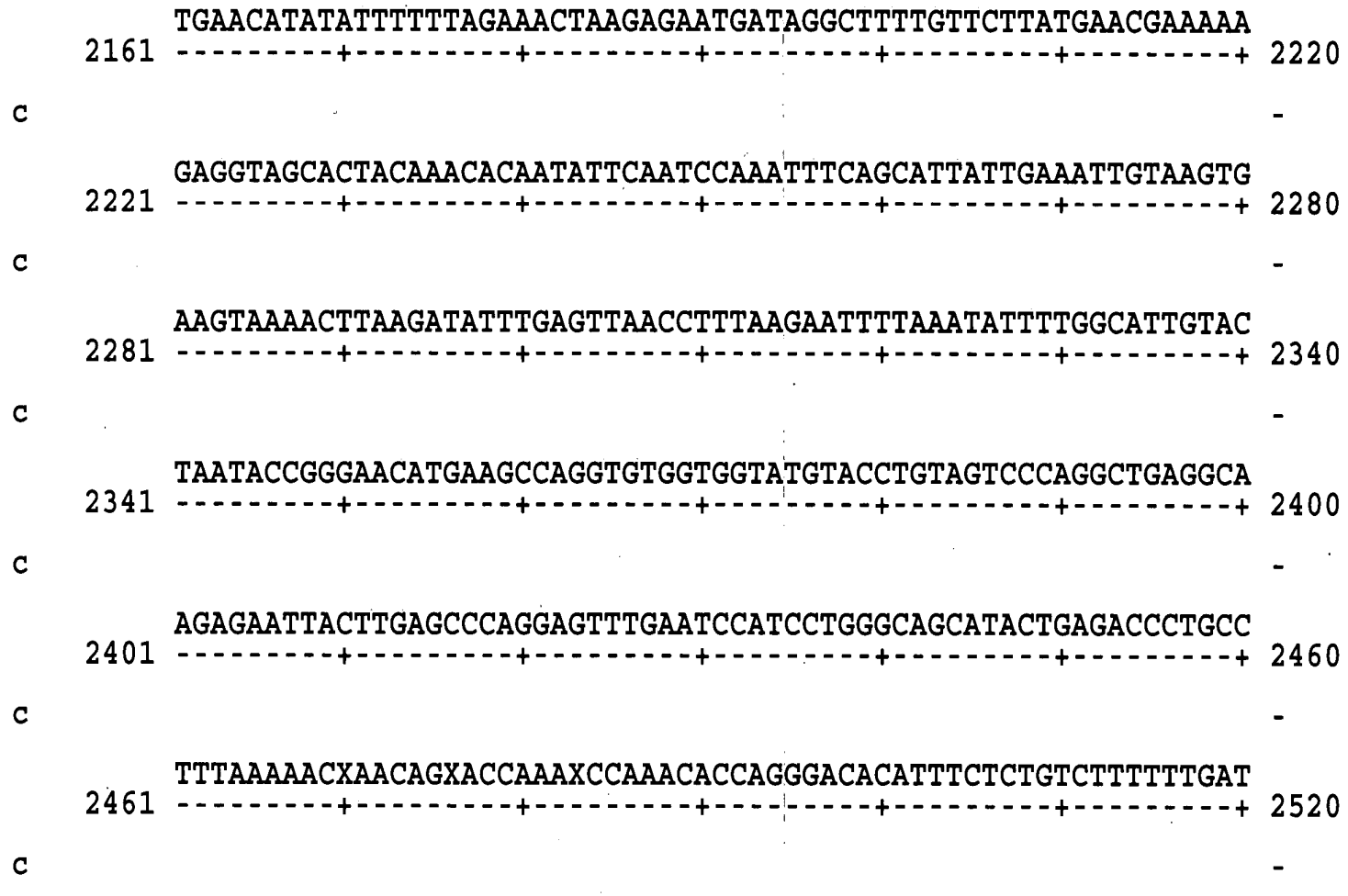


Fig. 2 (page 7 of 8)

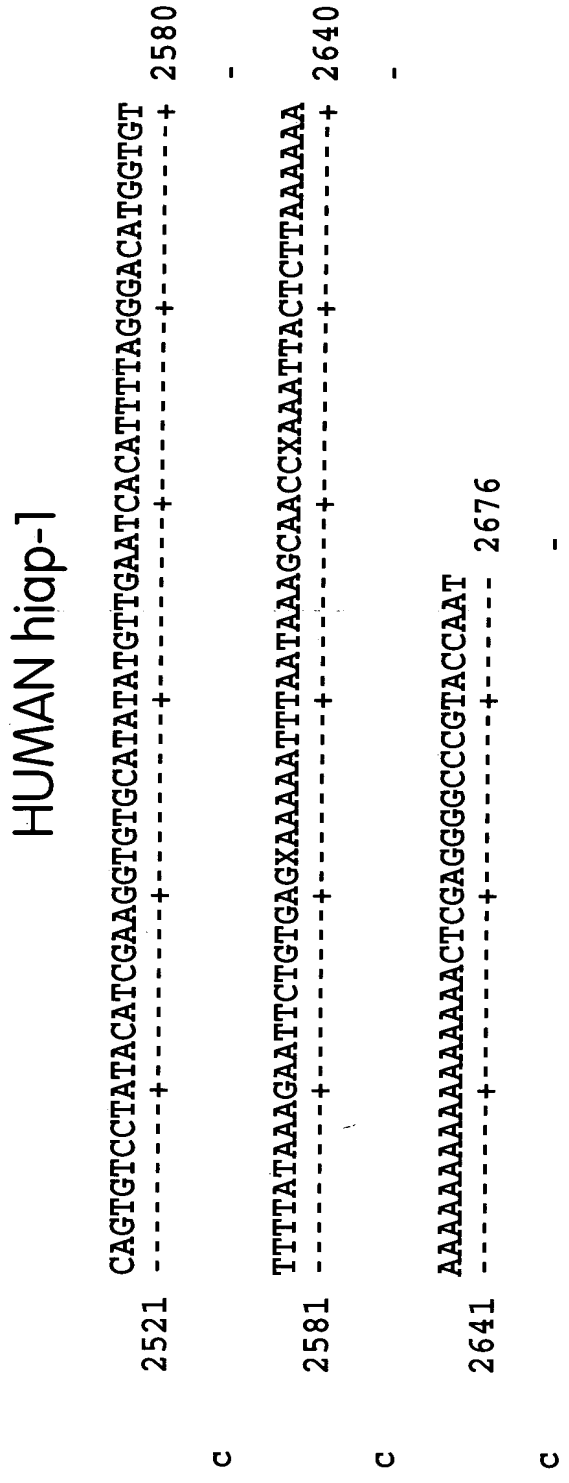


Fig. 2 (page 8 of 8)

# HUMAN hiap-2

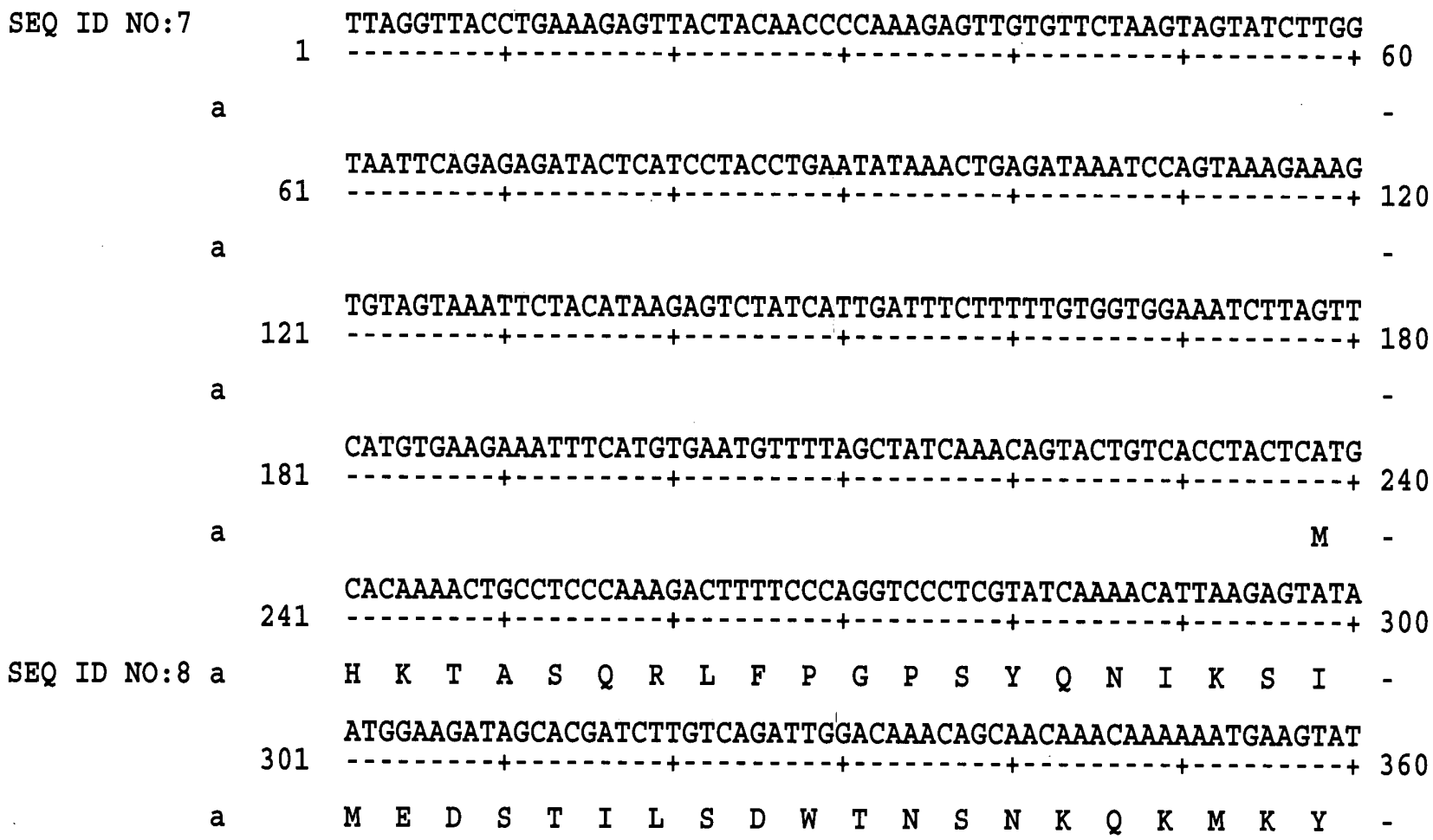


Fig. 3 (page 1 of 7)

# HUMAN hiap-2

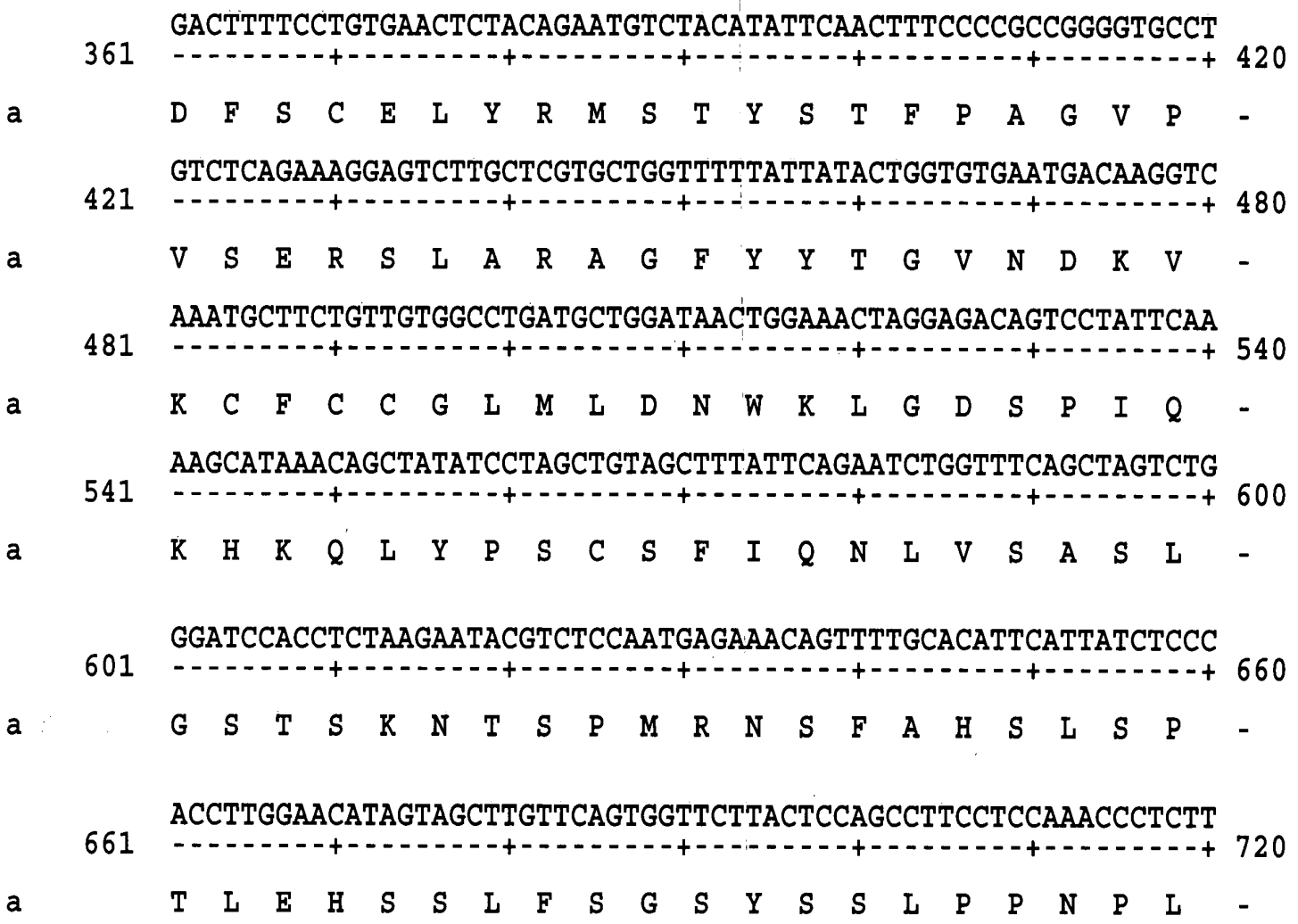


Fig. 3 (page 2 of 7)

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# HUMAN hiap-2

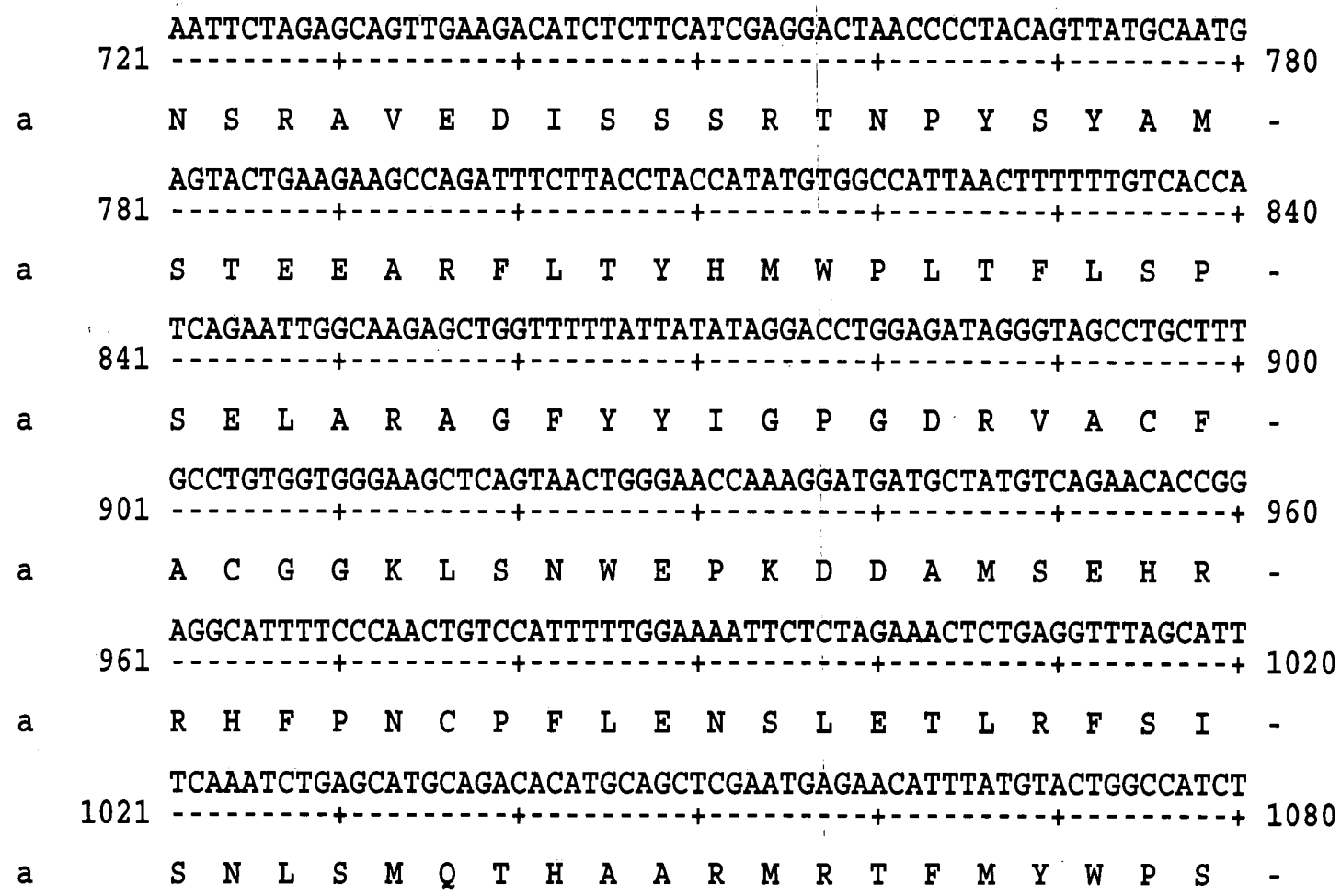


Fig. 3 (page 3 of 7)

# HUMAN hiap-2

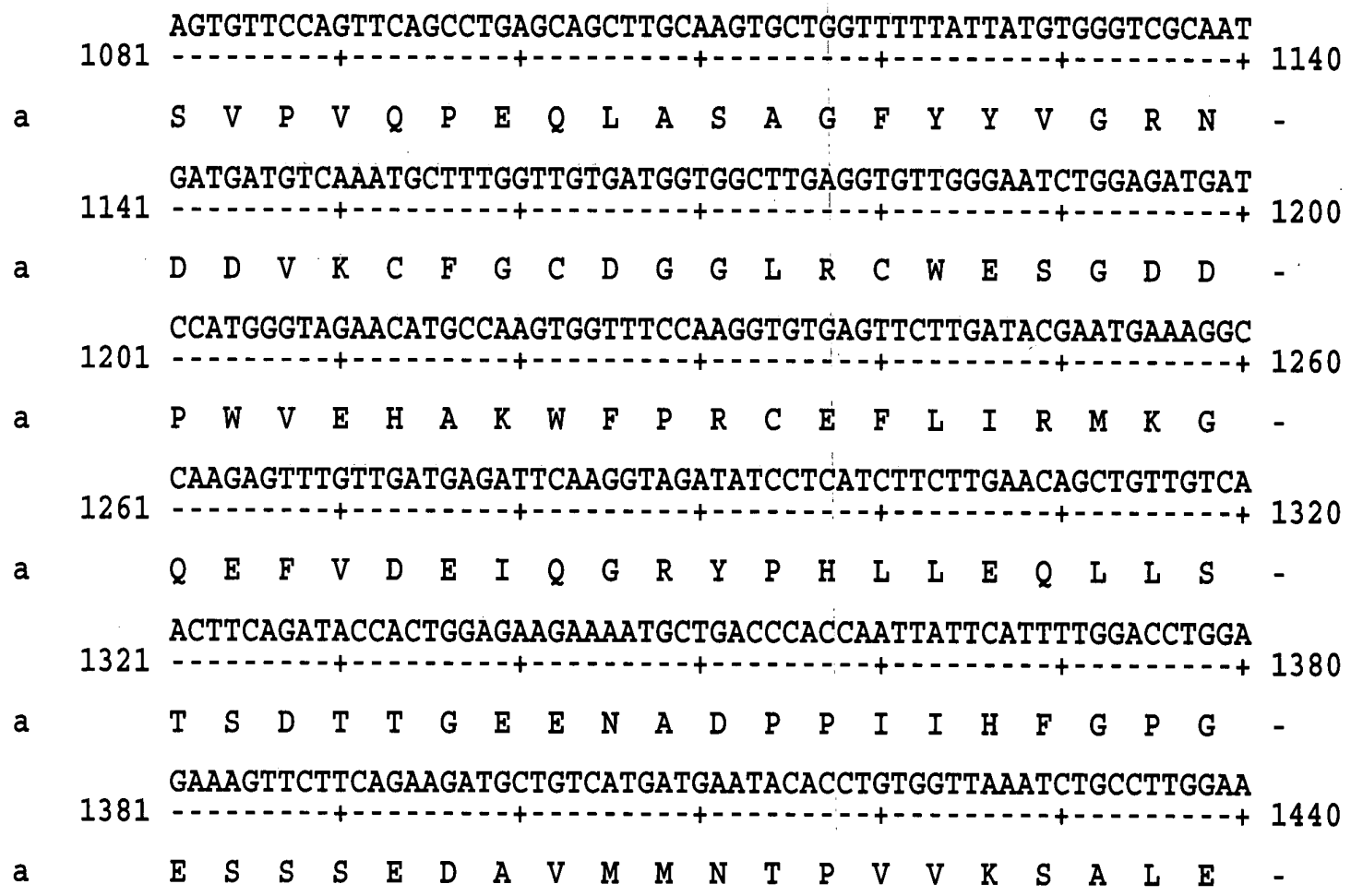


Fig. 3 (page 4 of 7)

# HUMAN hiap-2

Fig. 3 (page 5 of 7)

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# HUMAN hiap-2

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# HUMAN hiap-2

Fig. 3 (page 7 of 7)

# MOUSE xiap

Fig. 4 (page 1 of 6)

# MOUSE xiap

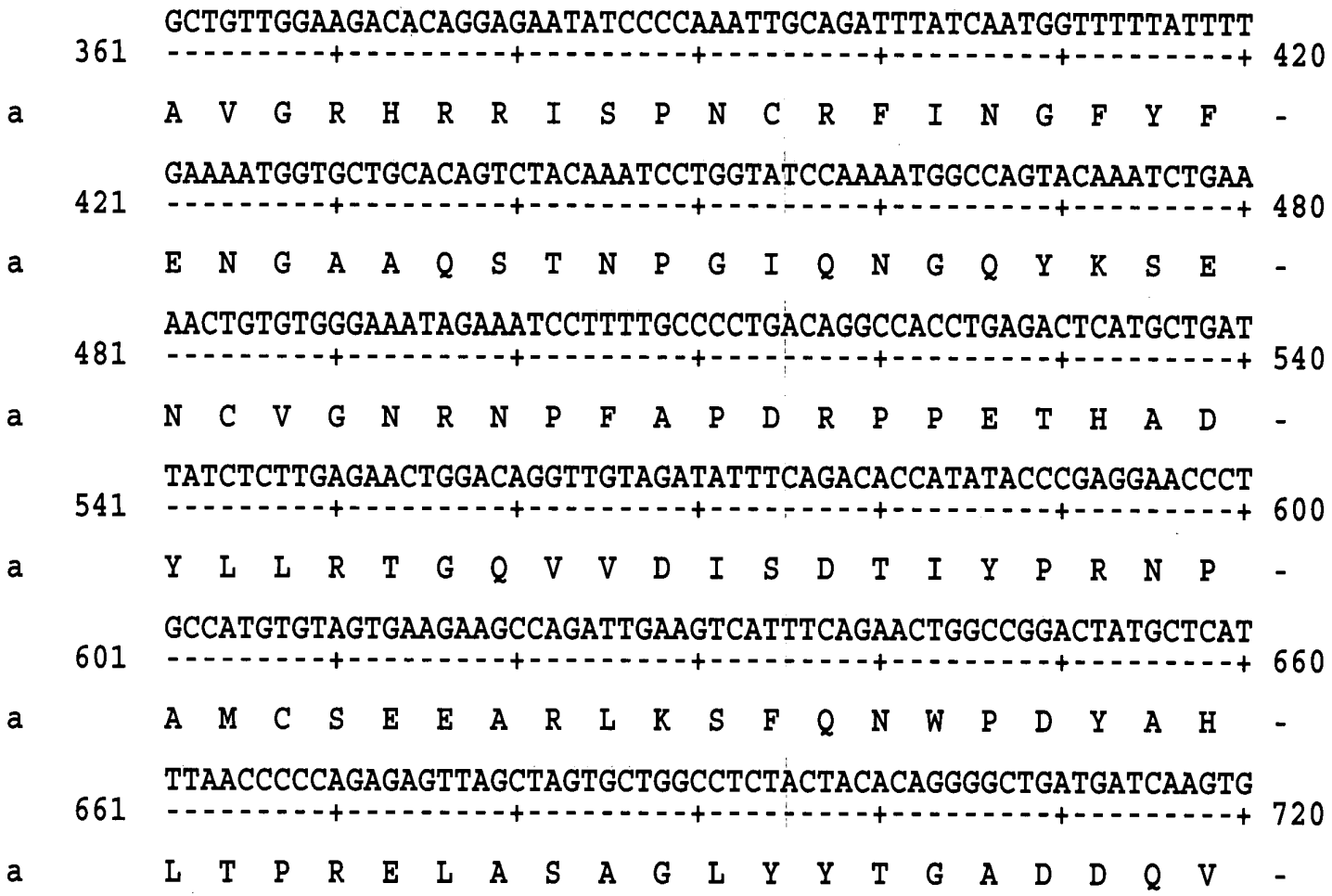


Fig. 4 (page 2 of 6)

Title: MAMMALIAN IAP GENE FAMILY, PRIMERS, PROBES ...
Applicant(s): Robert G. Korneluk et al.
Client/Matter No.: 07891/003005
Filing Date: September 1, 2000 Serial No.: 09/654,743
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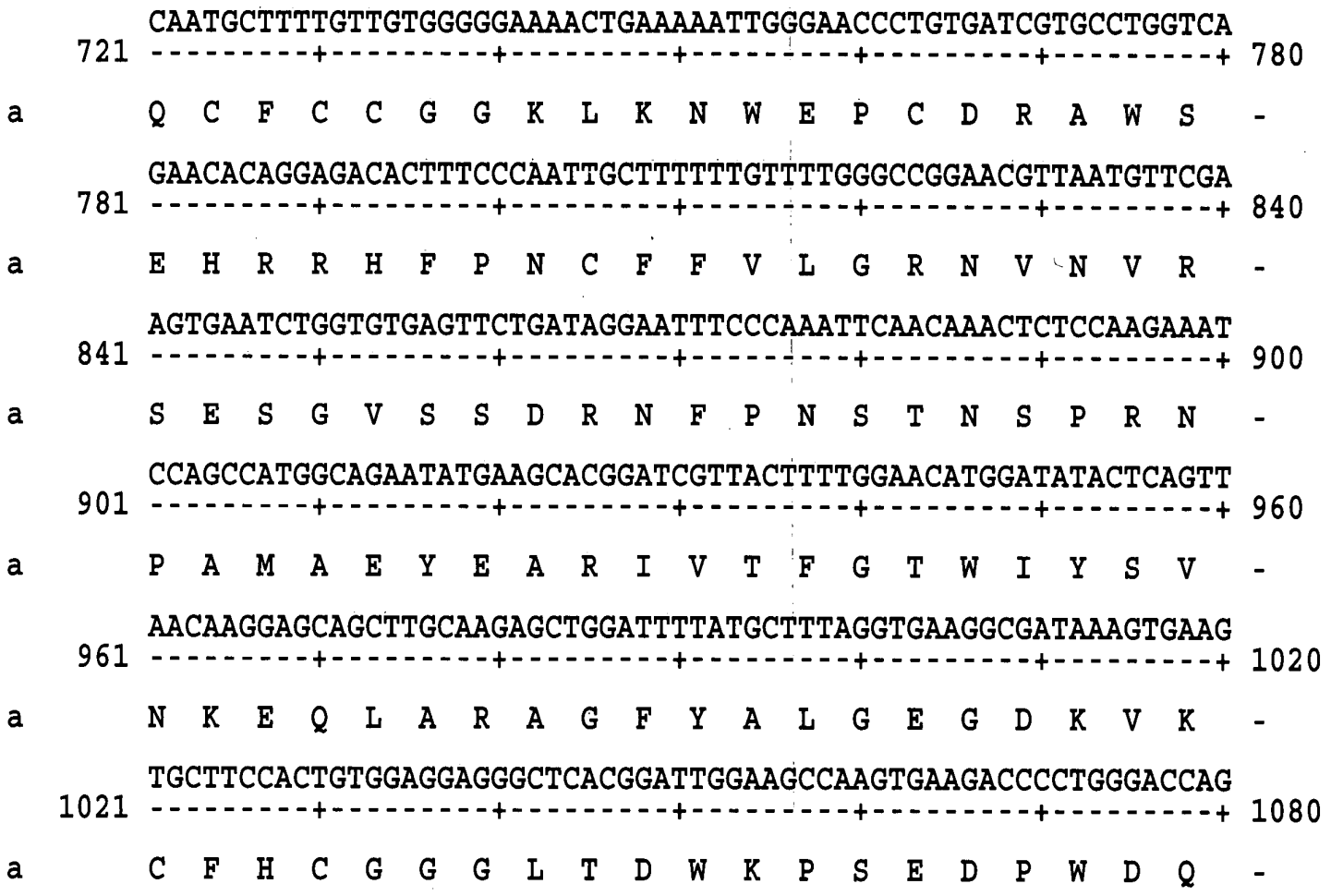


Fig. 4 (page 3 of 6)

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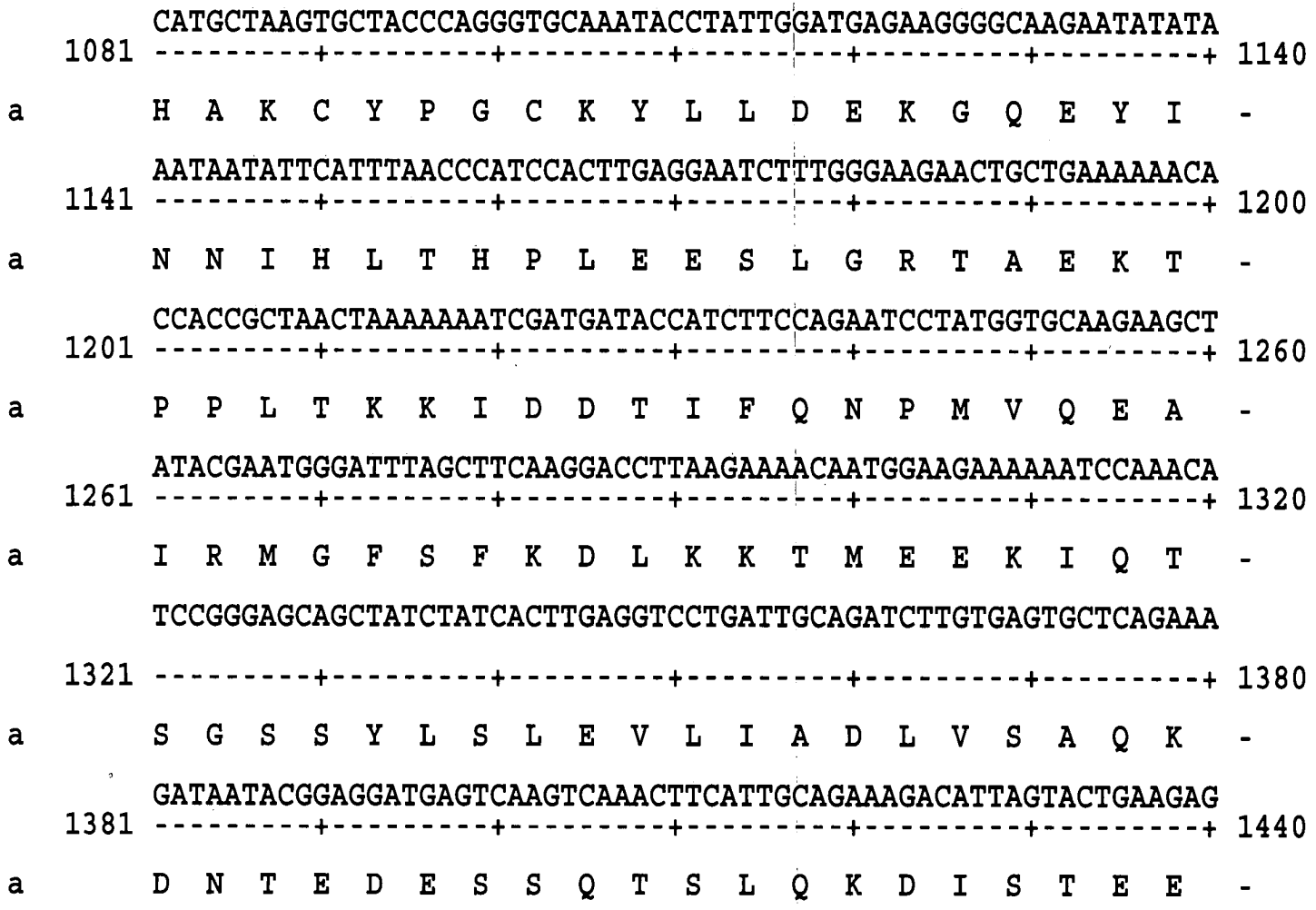


Fig. 4 (page 4 of 6)

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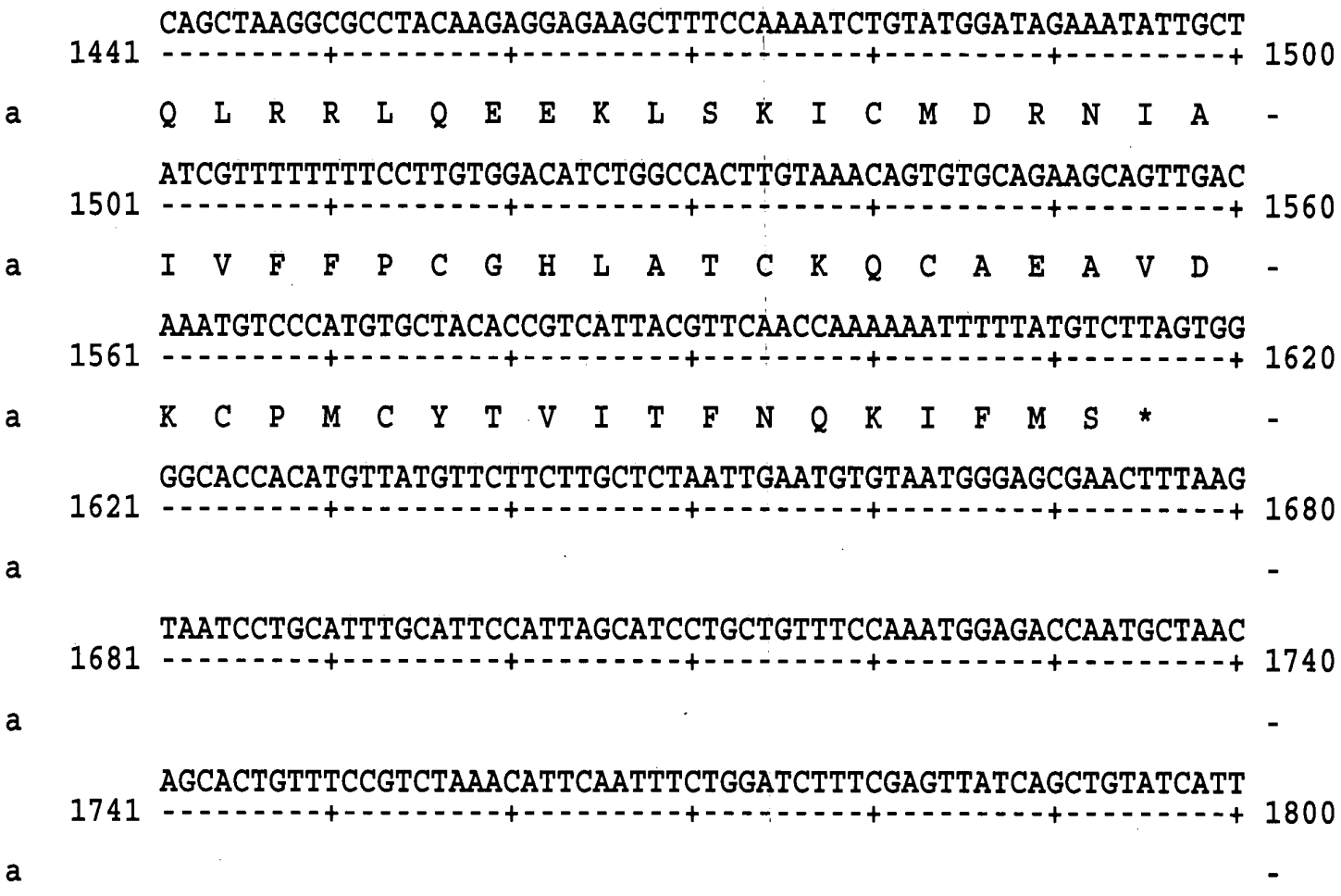


Fig. 4 (page 5 of 6)

# MOUSE xiap

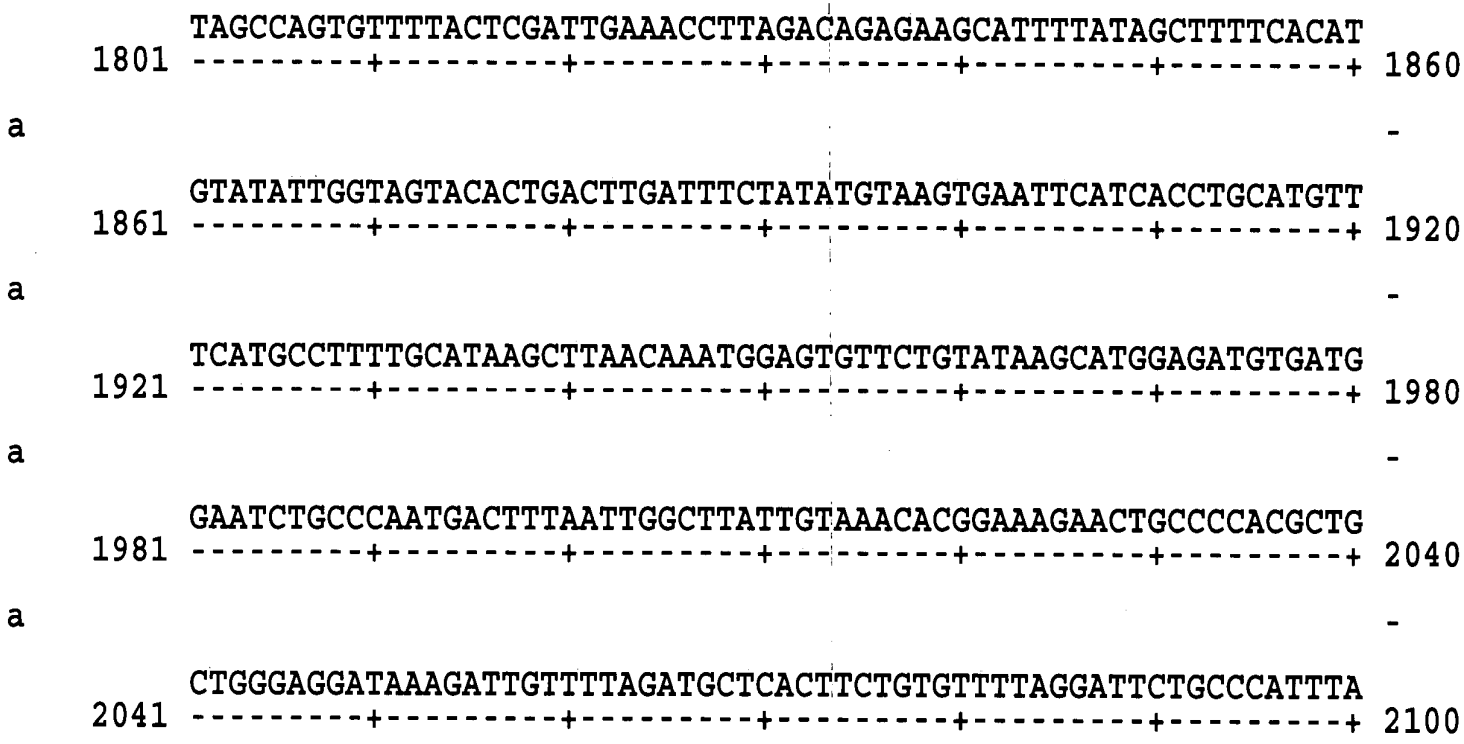


Fig. 4 (page 6 of 6)

# M-hiap-1

Fig. 5 (page 1 of 6)

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# M-hiap-1

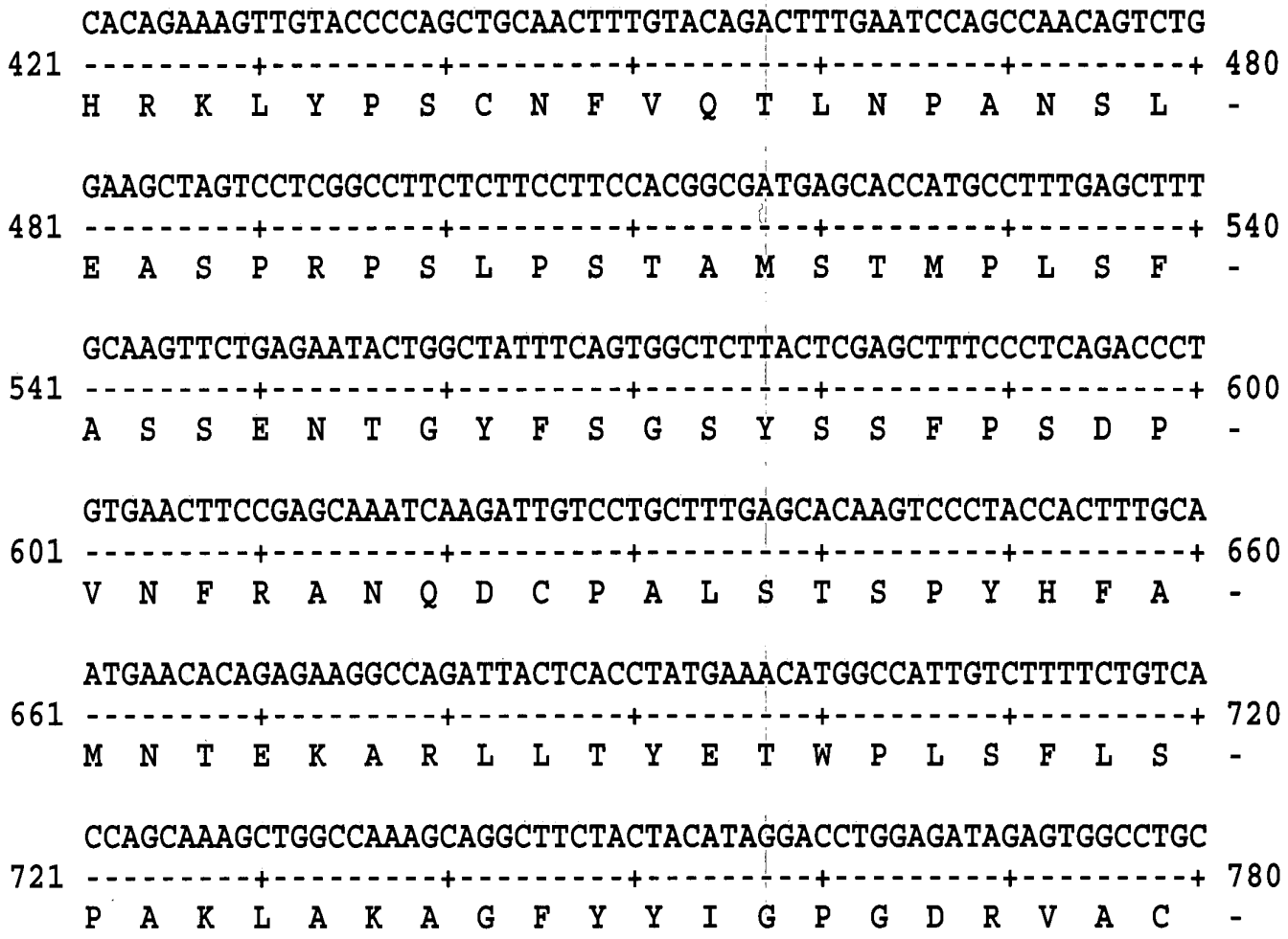


Fig. 5 (page 2 of 6)

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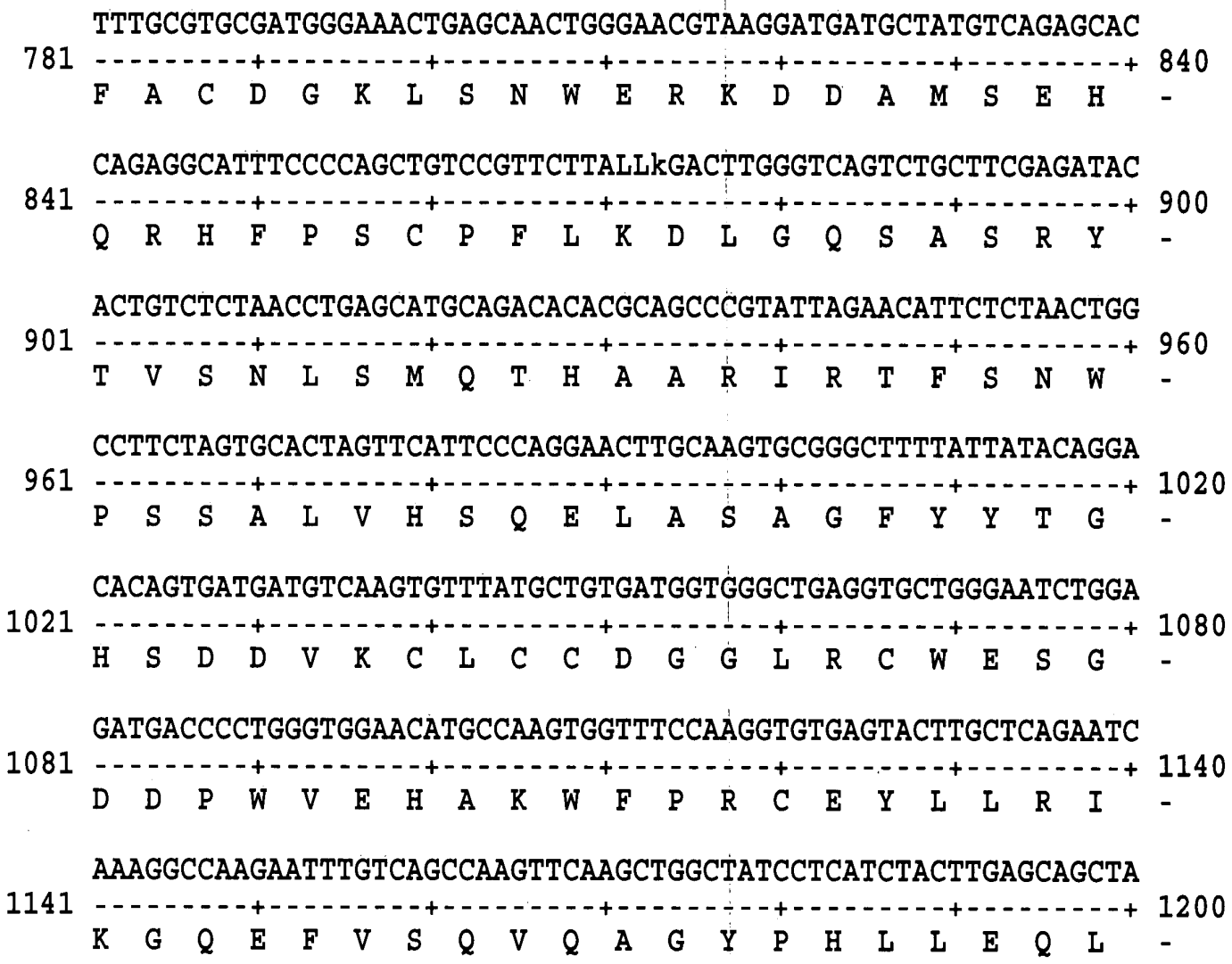


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# M-hiap-1

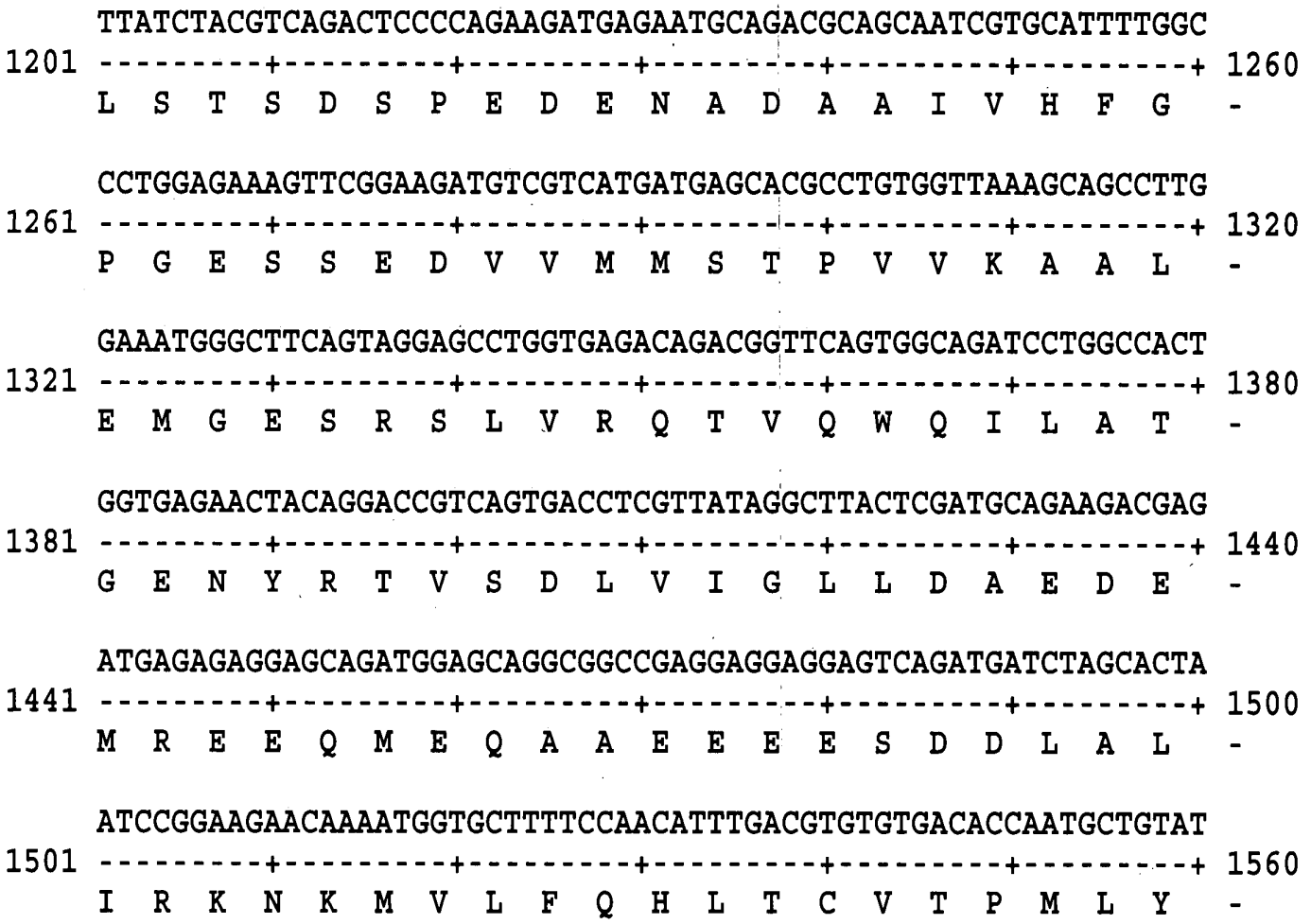


Fig. 5 (page 4 of 6)

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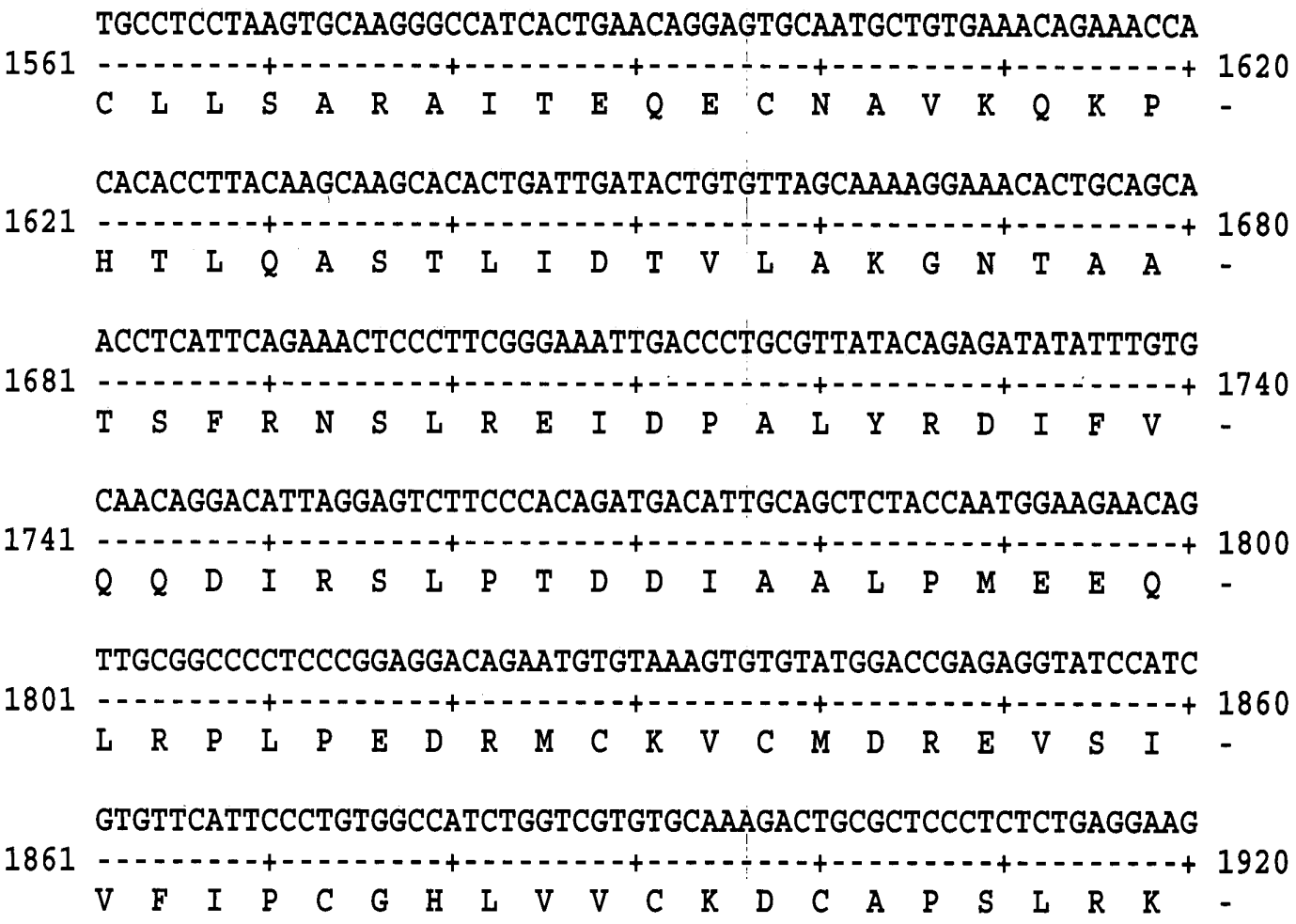
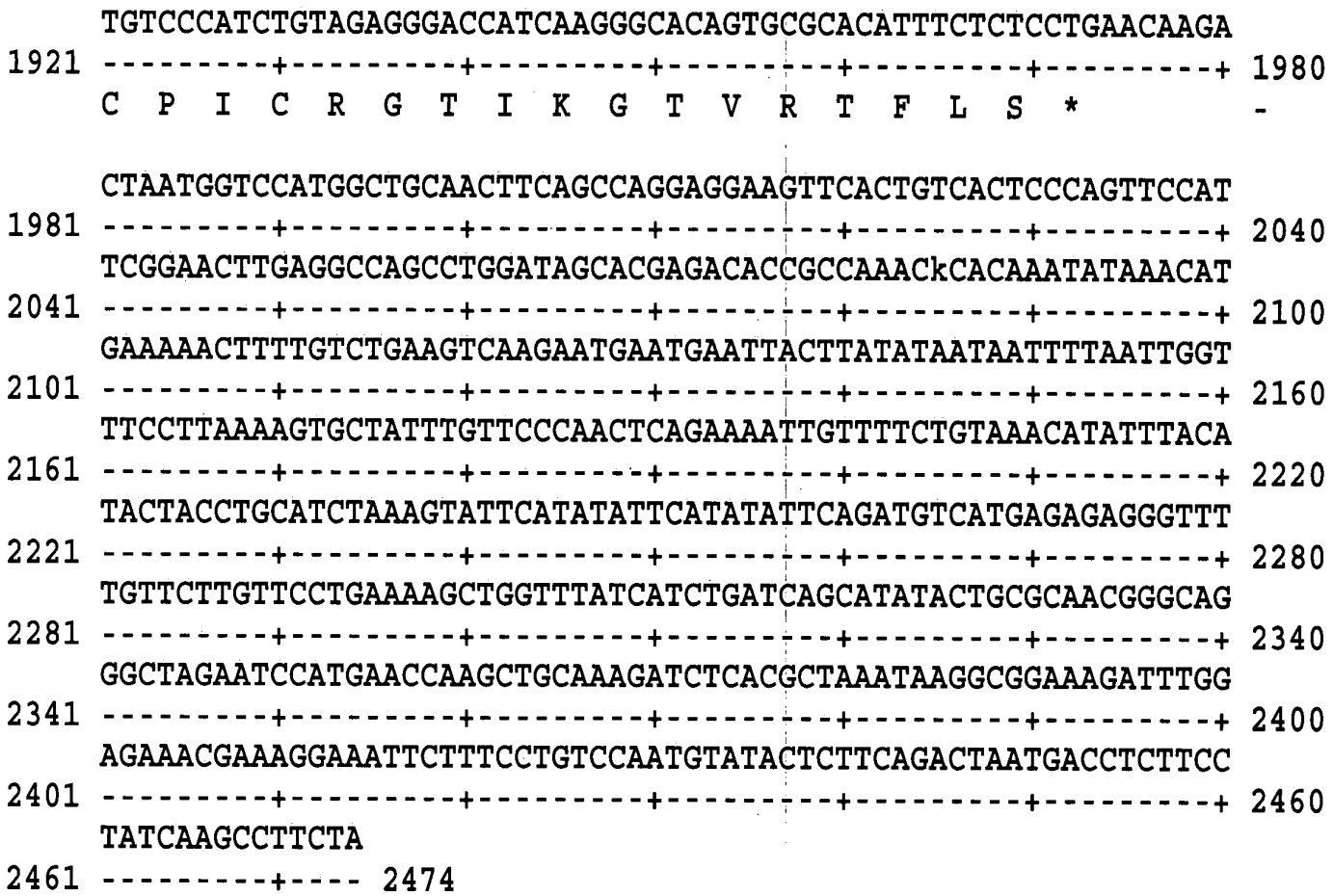



Fig. 5 (page 5 of 6)

# M-hiap-1

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# M-hiap-2

Fig. 6 (page 1 of 6)

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# M-hiap-2

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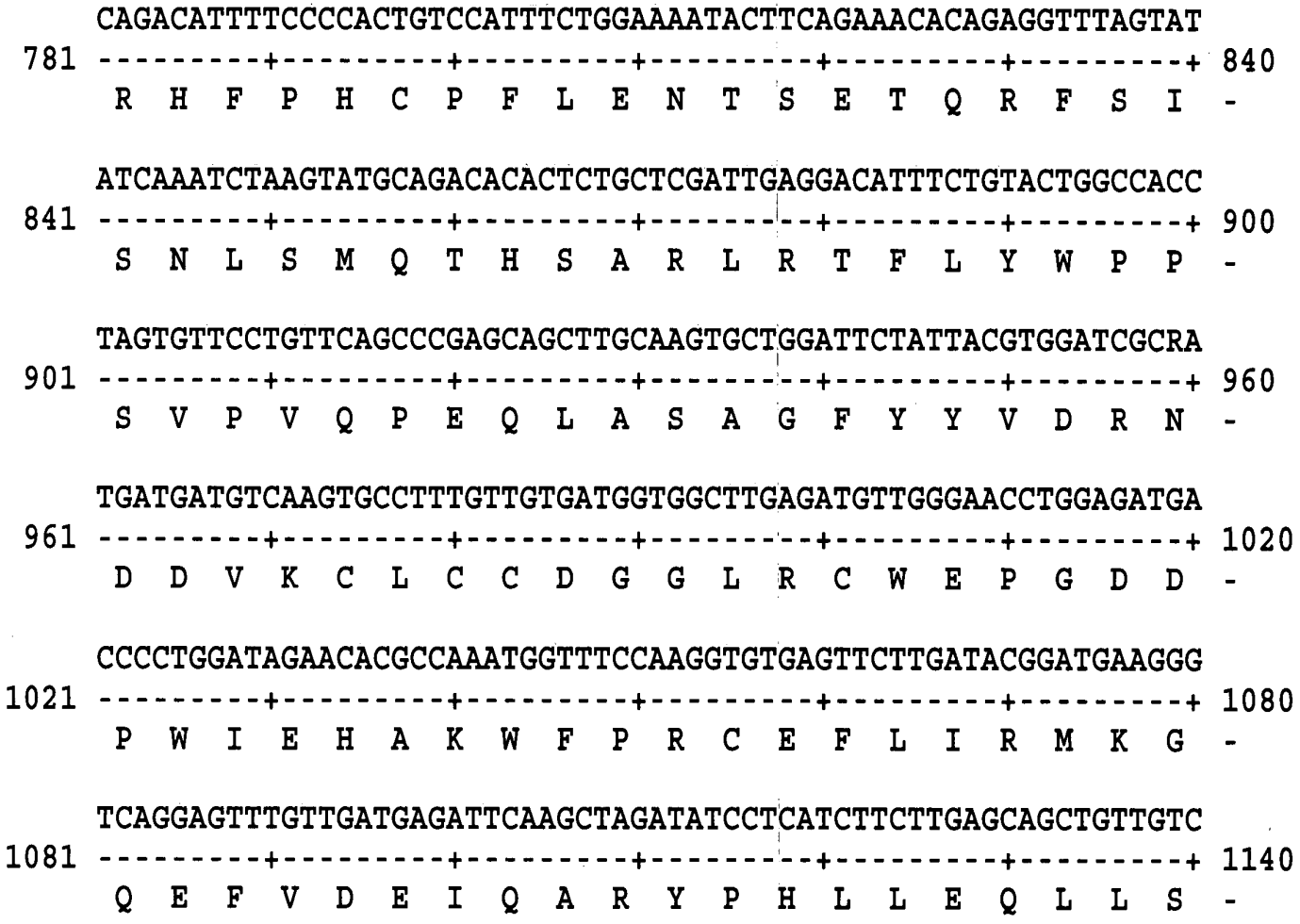
# M-hiap-2

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# M-hiap-2

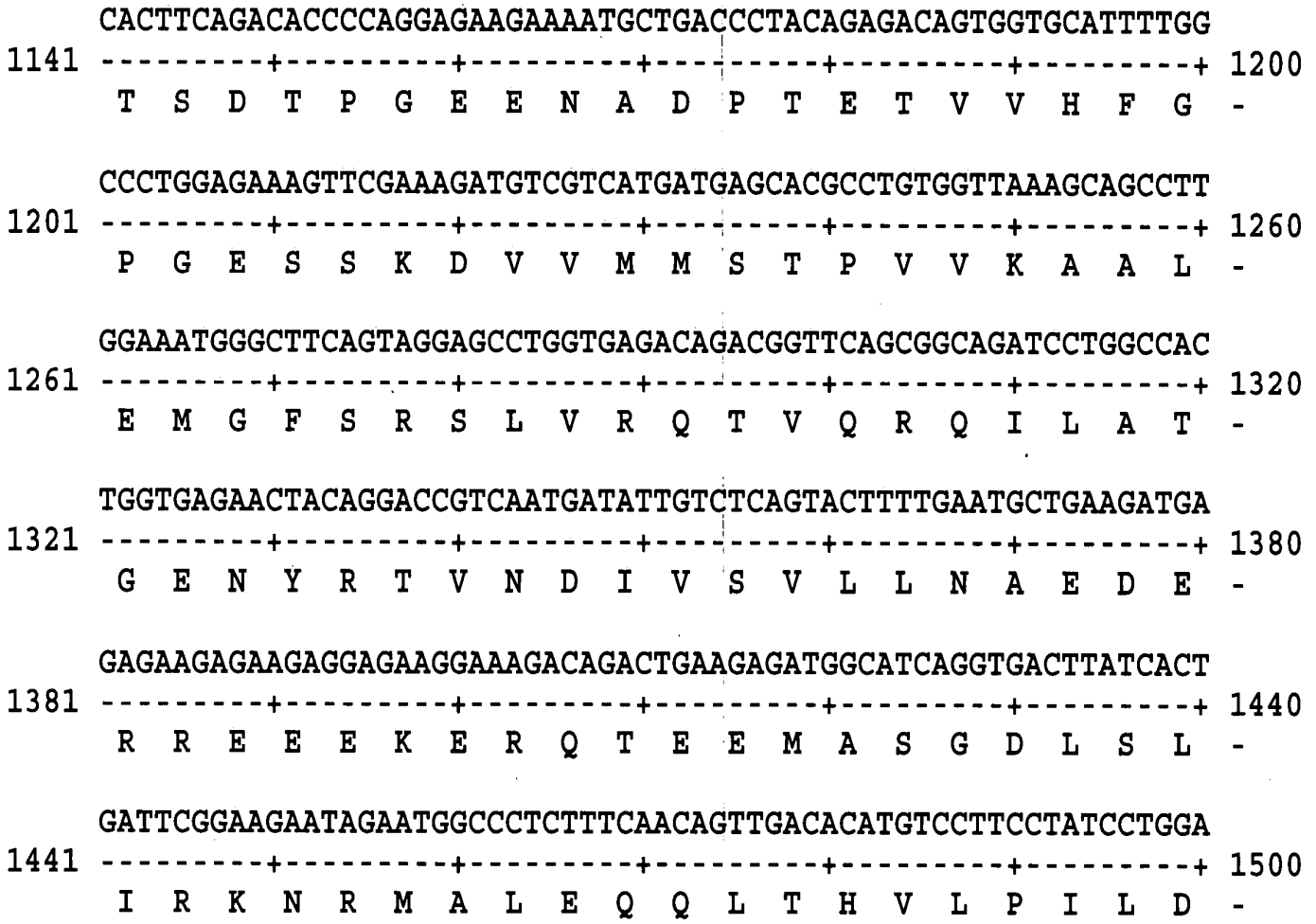


Fig. 6 (page 4 of 6)

# M-hiap-2

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1501 ---------+---------+---------+---------+---------+---------+ 1560
      N  L  L  E  A  S  V  I  T  K  Q  E  H  D  I  I  R  Q  K  T  -

     ACAGATACCCTTACAAGCAAGAGAGCTTATTGACACCGTTTTAGTCAAGGGAAATGCTGC
1561 ---------+---------+---------+---------+---------+---------+ 1620
      Q  I  P  L  Q  A  R  E  L  I  D  T  V  L  V  K  G  N  A  A  -

     AGCCAACATCTTCAAAAACTCTCTGAAGGGAATTGACTCCACGTTATATGAAAACTTATT
1621 ---------+---------+---------+---------+---------+---------+ 1680
      A  N  I  F  K  N  S  L  K  G  I  D  S  T  L  Y  E  N  L  F  -

     TGTGGAAAAGAATATGAAGTATATTCCAACAGAAGACGTTTCAGGCTTGTCATTGGAAGA
1681 ---------+---------+---------+---------+---------+---------+ 1740
      V  E  K  N  M  K  Y  I  P  T  E  D  V  S  G  L  S  L  E  E  -

     GCAGTTGCGGAGATTACAAGAAGAACGAACTTGCAAAGTGTGTATGGACAGAGAGGTTTC
1741 ---------+---------+---------+---------+---------+---------+ 1800
      Q  L  R  R  L  Q  E  E  R  T  C  K  V  C  M  D  R  E  V  S  -

     TATTGTGTTCATTCCGTGTGGTCATCTAGTAGTCTGCCAGGAATGTGCCCCTTCTCTAAG
1801 ---------+---------+---------+---------+---------+---------+ 1860
      I  V  F  I  P  C  G  H  L  V  V  C  Q  E  C  A  P  S  L  R  -
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# M-hiap-2

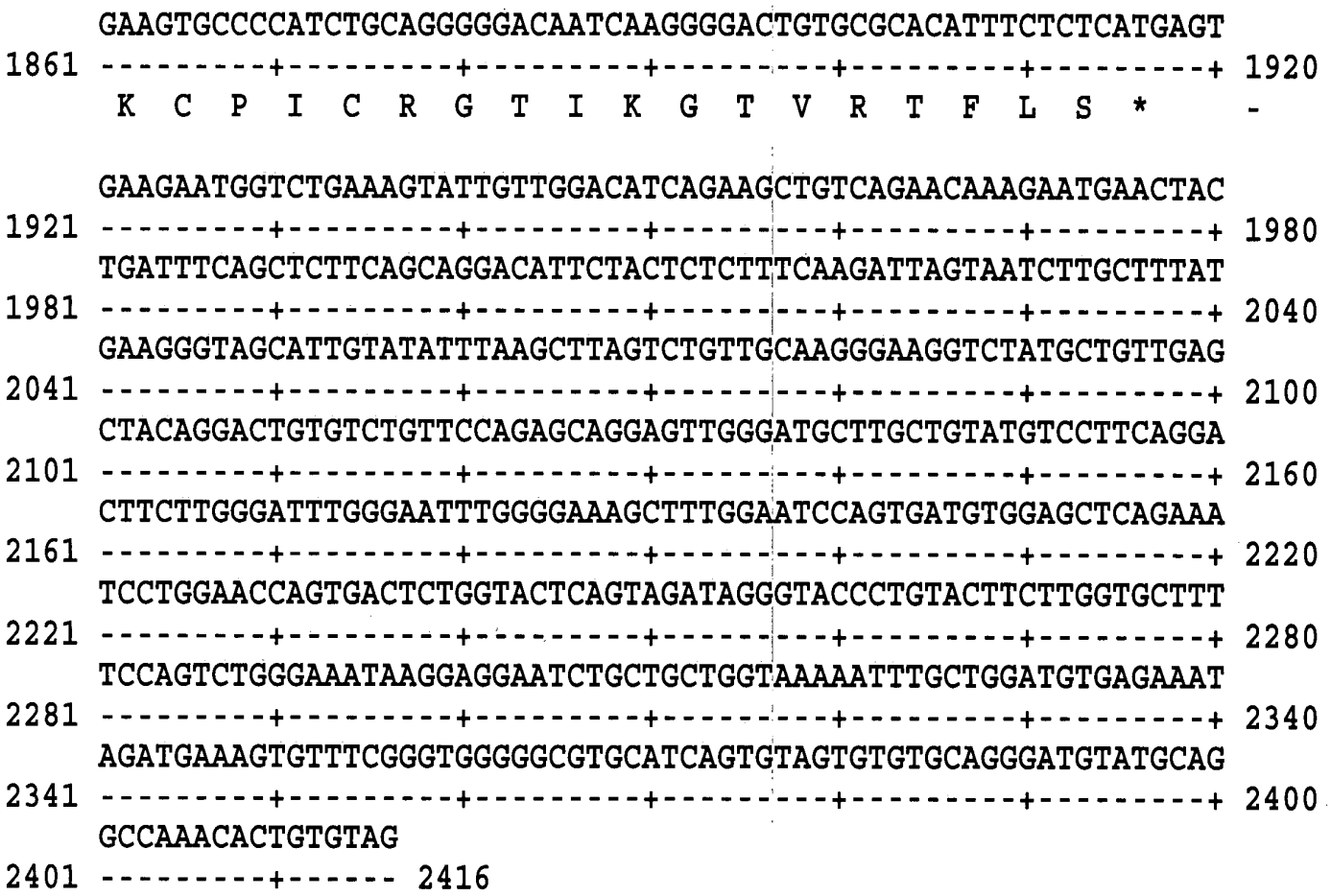


Fig. 6 (page 6 of 6)

## Alignment of BIR (Baculoviral IAP Repeats) Domains

**Baculovirus**

| | |
|---|---|
| Cp_iap | Cydia pomonella |
| Op_iap | Orgyia pseudotsugata |

**Human**

| | |
|---|---|
| xiap | IAP on X chromosome |
| hiap1, hiap2 | two different human IAP genes |

**Mouse**

| | |
|---|---|
| m-xiap | mouse homologue of human xiap gene |

**Insect**

| | |
|---|---|
| diap | Drosophilia IAP gene, not clearly a homologue of xiap or hiap |

**note on consensus:** The consensus line represents amino acids or very similar amino acids which are present in 14 of the 19 BIR sequences at each position. Capitalized residues are those that are in the consensus sequence.

Fig. 7

```
                                1                                                  68
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SEQ ID NO:14   Cp_iap-1    eevRLnTFek WPvsf.lspe tMAknGFYYl GrsDeVrCaf CkveimrWke gEdpaadHkk waPqCpFV
SEQ ID NO:15   diap-2      eanRLvTFkd WPnpn.iLpq aLAkAGFYYl nrlDhVkCvw CngviakWek nDnafeeHkr ffPqCprV
SEQ ID NO:16   m-xiap-1    efnRLkTFan FPssspvsas tLArAGFLYt GegDtVqCFs ChaaidrWqy gDsavgrHrr isPnCrFI
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SEQ ID NO:18   hiap1-1     elyRMsTYst FPagvpvser sLArAGFYYt GvnDkVkCFc CglmldnWkr gDsptekHkk lyPsCrFV
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SEQ ID NO:20   m-xiap-2    eeaRLksFqn WPdyahltpr eLAsAGLYYt GadDqVqCFc CggklknWep cDrawseHrr hfPnCfFv
SEQ ID NO:21   xiap-2      eeaRLksFqn WPdyahltpr eLAsAGLLYt GigDqVqCFc CggklknWep cDrawseHrr hfPnCfFV
SEQ ID NO:22   hiap1-2     enaRLlTFqt WP.lLflspt dLArAGFYYi GpgDrVaCFa CggklsnWep kDnamseHlr hfPkCpFI
SEQ ID NO:23   hiap2-2     eeaRFlTYhm WP.lLflsps eLArAGFYYi GpgDrVaCFa CggklsnWep kDdamseHrr hfPnCpFl
SEQ ID NO:24   m-xiap-3    yeaRivTFgt Wiysv..nke qLArAGFYal GegDkVkCFh CgggltdWkp sEdpwdqHak cyPgCkYl
SEQ ID NO:25   xiap-3      yeaRifTFgt Wiysv..nke qLArAGFYal GegDkVkCFh CgggltdWkp sEdpweqHak wyPgCkYl
SEQ ID NO:26   hiap1-3     haaRFkTFfn WPssvlvnpe qLAsAgFYYv GnsDdVkCFc CdgglrcWes gDdpwvqHak wfPrCeYl
SEQ ID NO:27   hiap2-3     haaRMrTFmy WPssvpvqpe qLAsAGFYYv GrnDdVkCFg CdgglrcWes gDdpwveHak wfPrCeFl
SEQ ID NO:28   Op_iap-2    eaaRLrTFae WPrglkqrpe eLAeAGFFYt GqgDktrCFc CdgglkdWep dDapwqqHar wydrCeYV
SEQ ID NO:29   Cp_iap-2    eaaRvksFhn WPrcmkqrpe qMAdAGFFYt GygDntkCFy CdgglkdWep eDvpweqHvr widrCaYV
SEQ ID NO:30   diap-3      vdaRLrTFtd WPisniqpas aLAqAGLYYq kigDqVrCFh CniglrsWqk eDepwieHak wsPkCqFV
SEQ ID NO:31   diap-1      esvRLaTFge WPlnapvsae dLvanGFF.. GtwmeaeCdf ChvridrWey gDlvaerHrr ssPiCsmV
SEQ ID NO:2    Consensus   ---RL-TF-- WP-------- -LA-AGFYY- G--D-V-CF- C------W-- -D-----H-- --P-C-FV
```



Title: MAMMALIAN IAP GENE FAMILY, PRIMERS, PROBES ...
Applicant(s): Robert G. Korneluk et al.
Client/Matter No.: 07891/003005
Filing Date: September 1, 2000 Serial No.: 09/654,743
Page 41 of 61 Customer No.: 21559

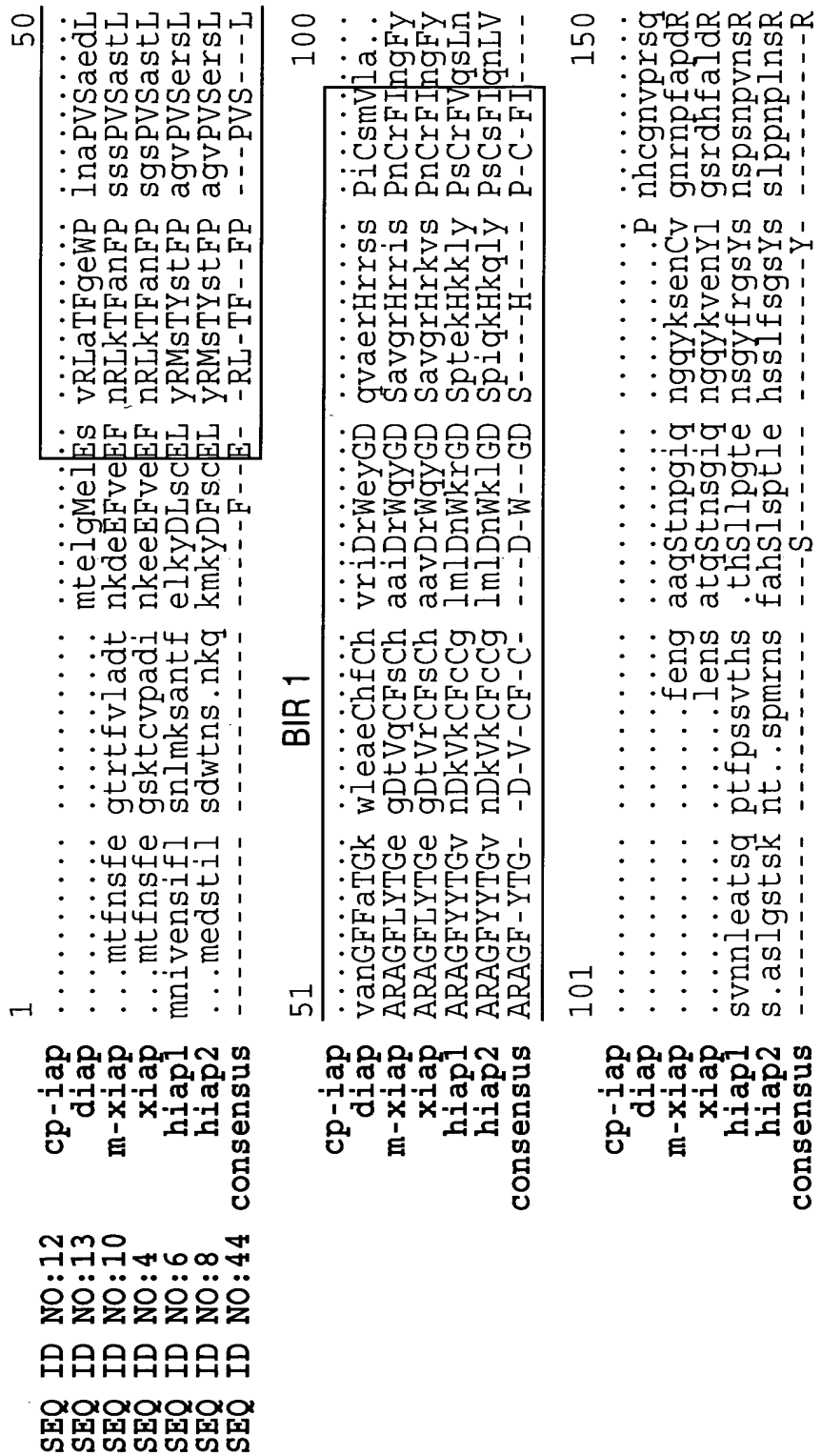


Fig. 8 (page 1 of 5)

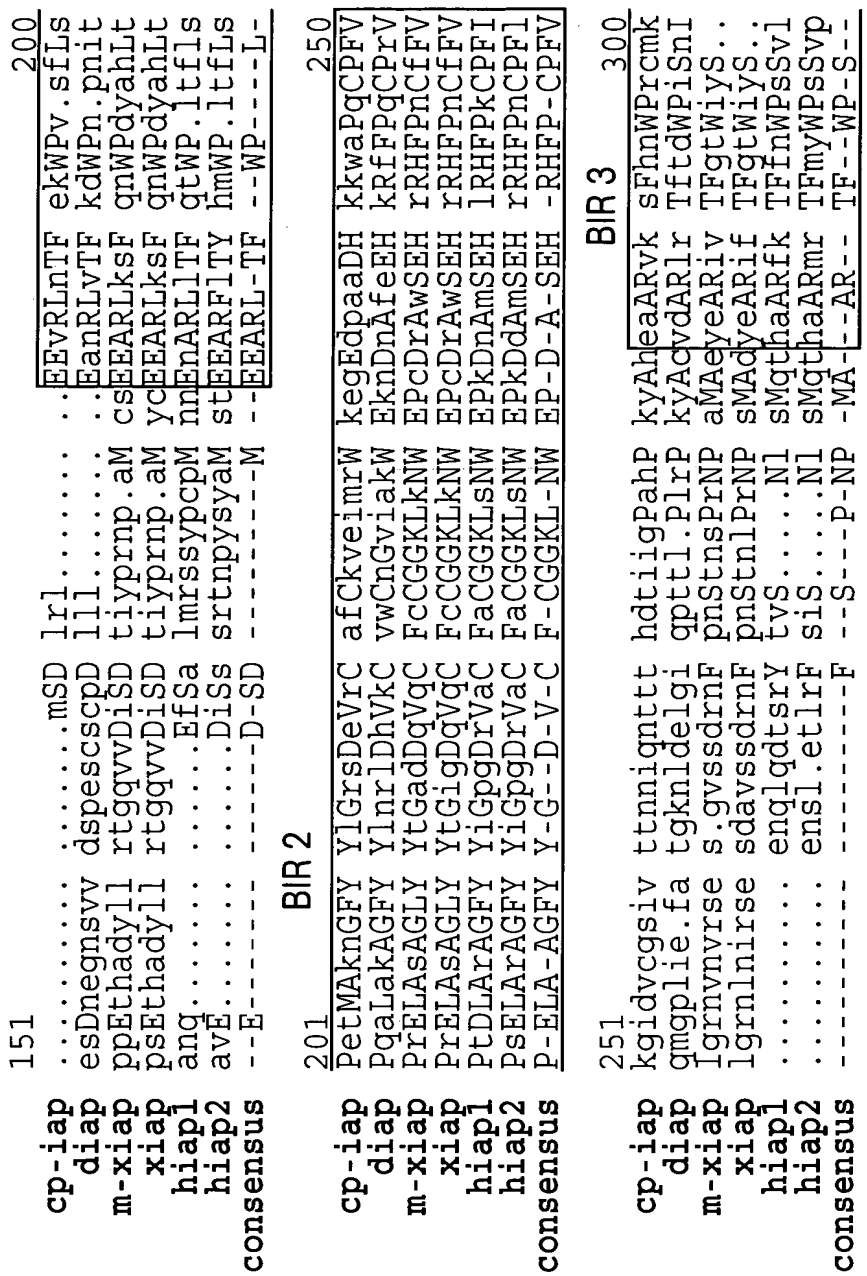


Fig. 8 (page 2 of 5)

Fig. 8 (page 3 of 5)

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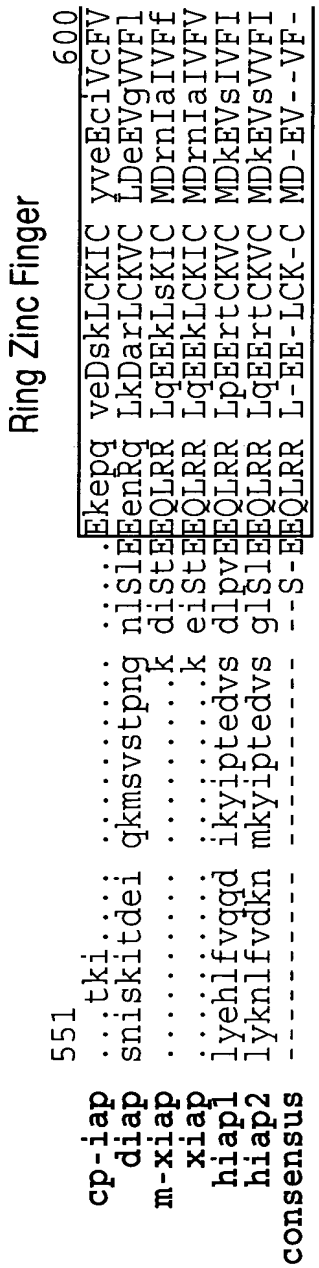


Fig. 8 (sheet 5 of 5)

## Alignment of RZF (Ring Zinc Finger) Domains

**Baculovirus**
- Cp_iap — Cydia pomonella
- Op_iap — Orgyia pseudotsugata

**Human**
- xiap — IAP on X chromosome
- hiap1, hiap2 — two different human IAP genes

**Mouse**
- m-xiap — mouse homologue of human xiap gene

**Insect**
- diap — Drosophilia IAP gene, not clearly a homologue of xiap or hiap

**note on consensus:** The consensus line represents amino acids or very similar amino acids which are present in 6 of the 7 RZF sequences at each position. Capitalized residues are those that are in the consensus sequence.

```
                                1                                   46
SEQ ID NO:32 hiap2      Eqlrrlqeer tCKVCMdkev sVvFiPCGHl vvCqeCApel rkCPiC
SEQ ID NO:33 hiap1      Eqlrrlpeer tCKVCMdkev sIvFiPCGHl w CkdCApsl rkCPiC
SEQ ID NO:34 m-xiap     Eqlrrlqeek lsKICMdrni aIvFfPCGHl atCkqCAeav dkCPmC
SEQ ID NO:35 xiap       Eqlrrlqeek lCKICMdrni aIvFvPCGHl vtCkqCAeav dkCPmC
SEQ ID NO:36 diap       Eenrqlkdar lCKVCLdeev gVvFlPCGHl atCnqCApev anCPmC
SEQ ID NO:37 Cp_iap     EkepgveDsk lCKICyveec iVcFvPCGHv vaCakCAlsv dkCPmC
SEQ ID NO:38 Op_iap     aveaevaDdr lCKICLgack tVcFvPCGHv vaCgkCAagv ttCPvC
SEQ ID NO:1  consensus  E------E-- -CKICM---- -V-F-PCGH- --C--CA--- --CP-C
```

Fig. 9



Title: MAMMALIAN IAP GENE FAMILY, PRIMERS, PROBES ...
Applicant(s): Robert G. Korneluk et al.
Client/Matter No.: 07891/003005
Filing Date: September 1, 2000 Serial No.: 09/654,743
Page 47 of 61 Customer No.: 21559

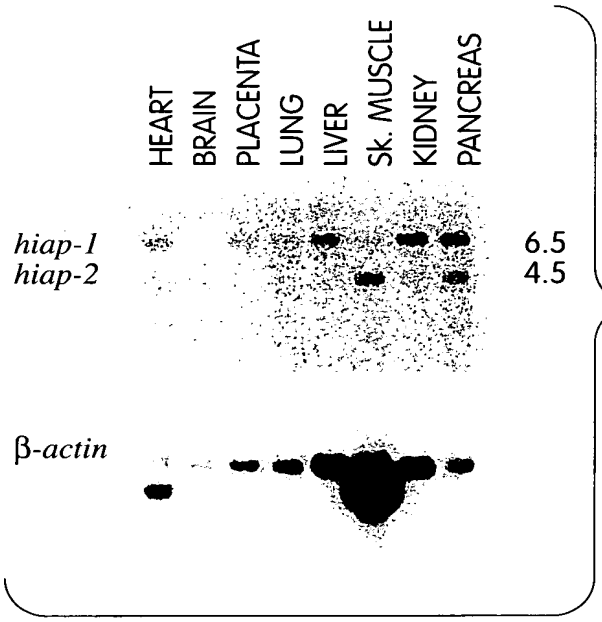


Fig. 10A

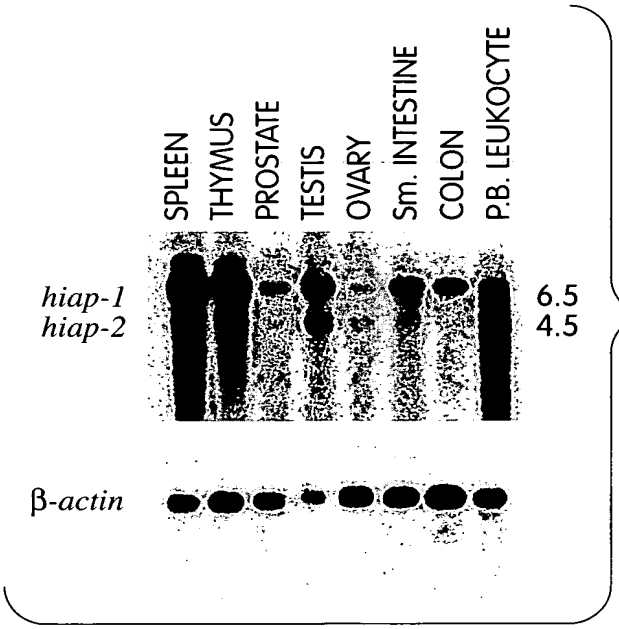


Fig. 10B

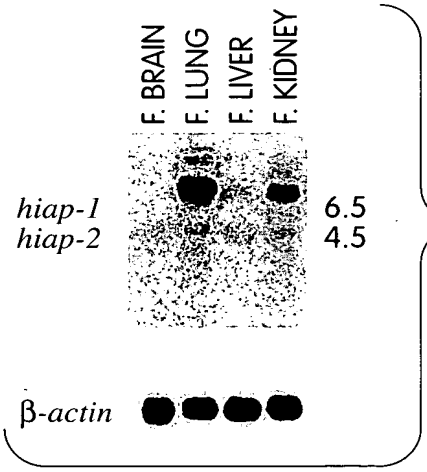


Fig. 10C

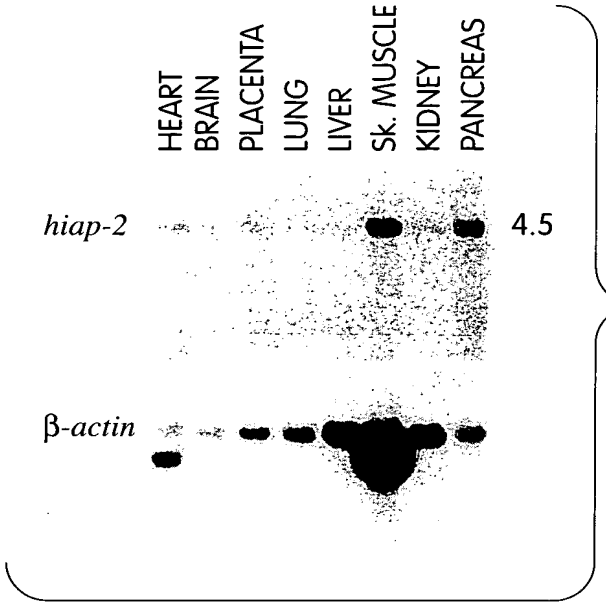


Fig. 11A

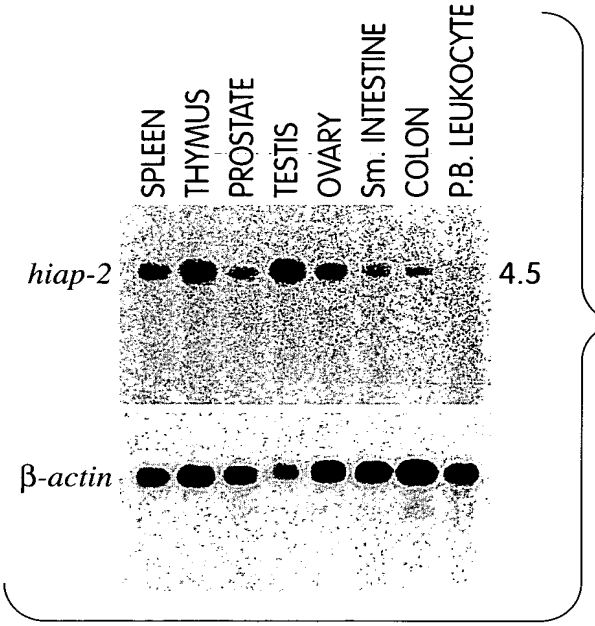


Fig. 11B

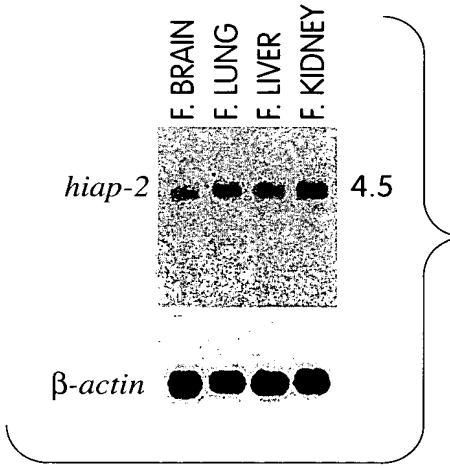


Fig. 11C

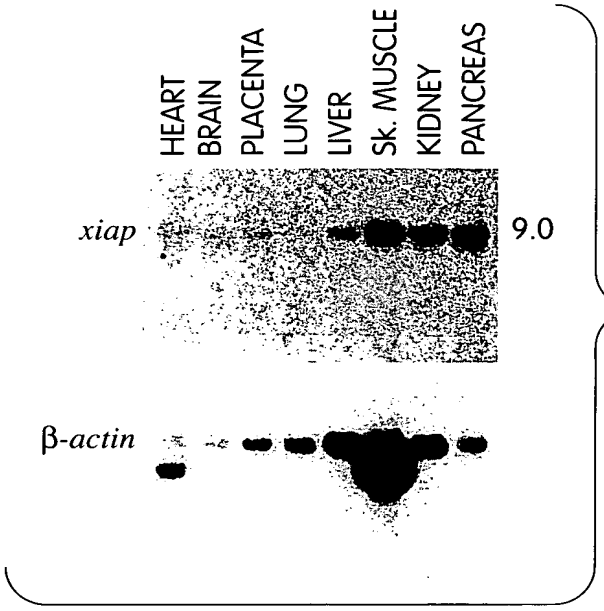


Fig. 12A

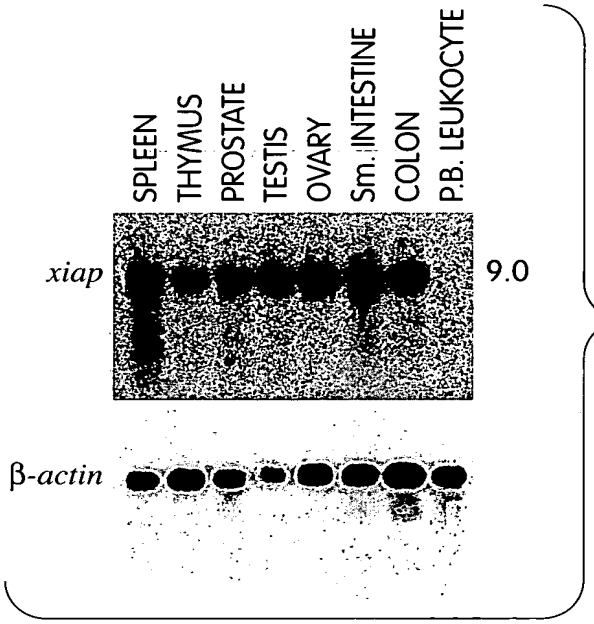


Fig. 12B

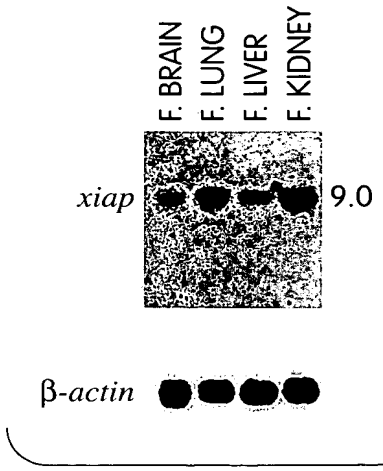


Fig. 12C

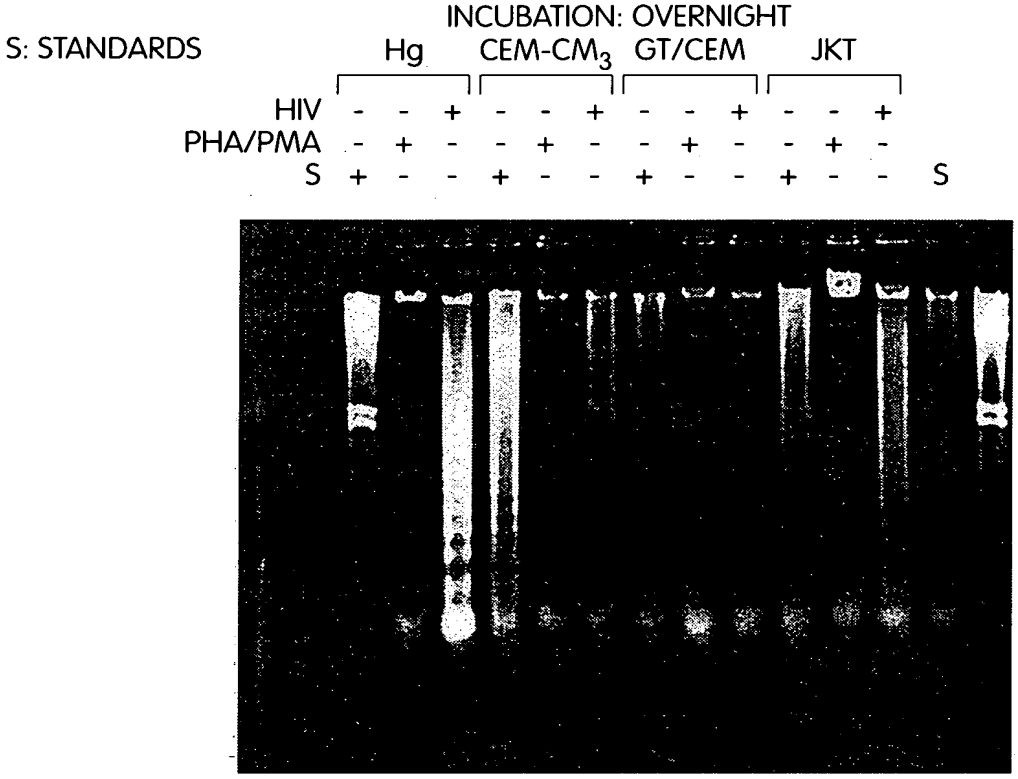


Fig. 13A

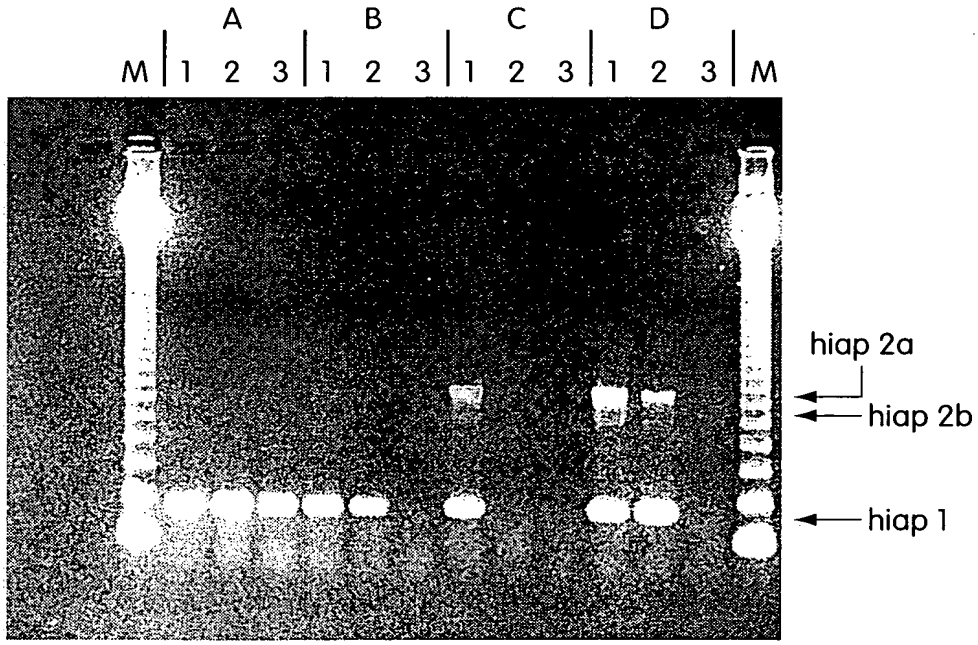


Fig. 13B

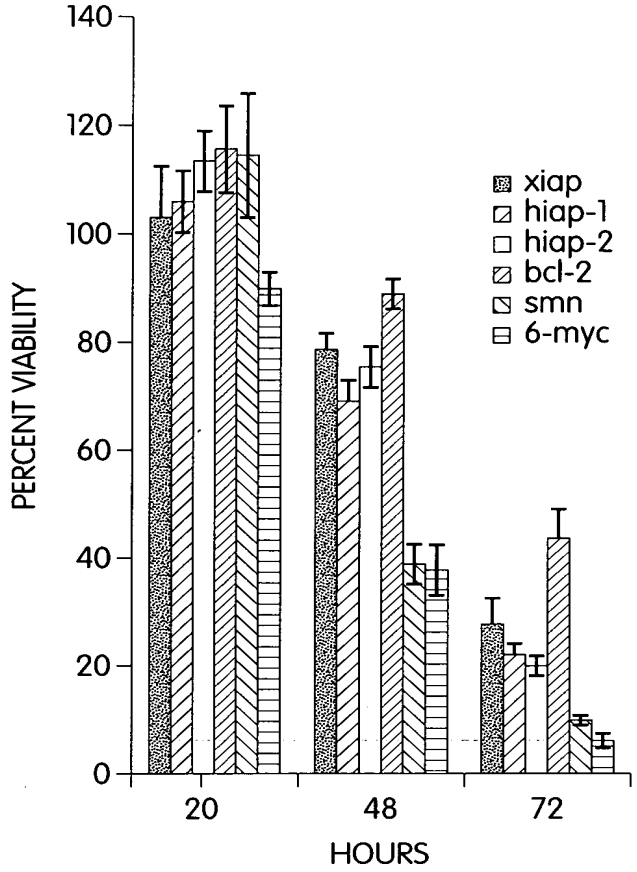


Fig. 14A

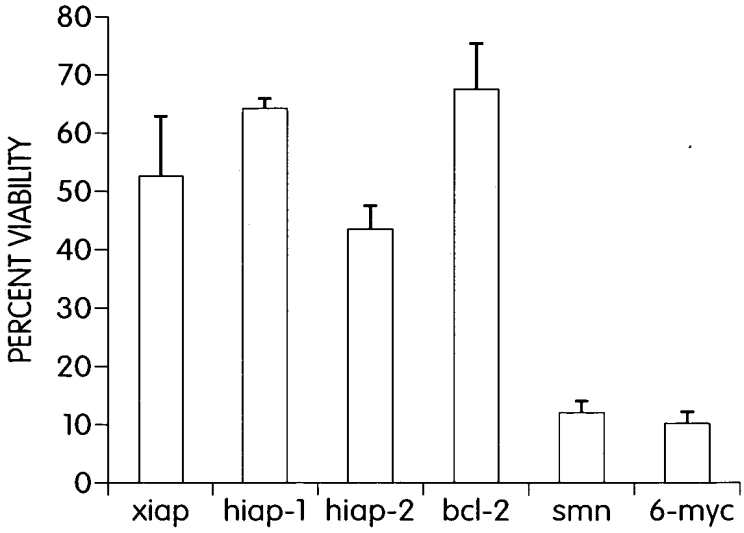


Fig. 14B

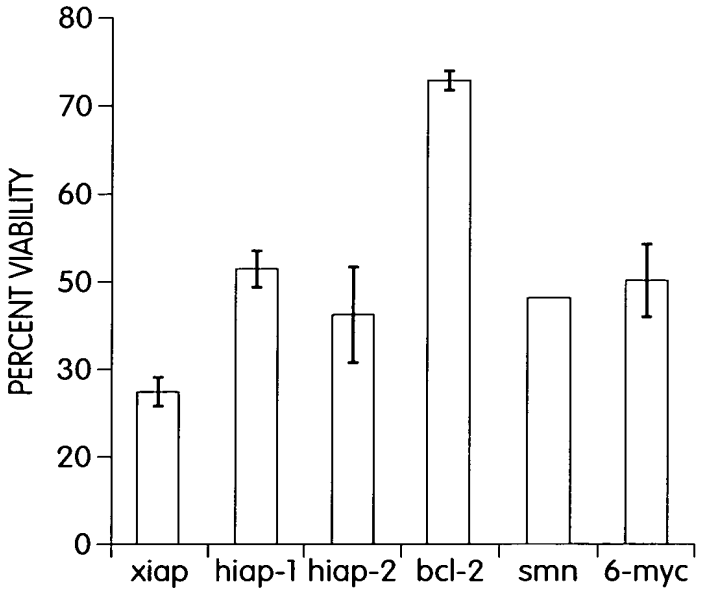


Fig. 14C

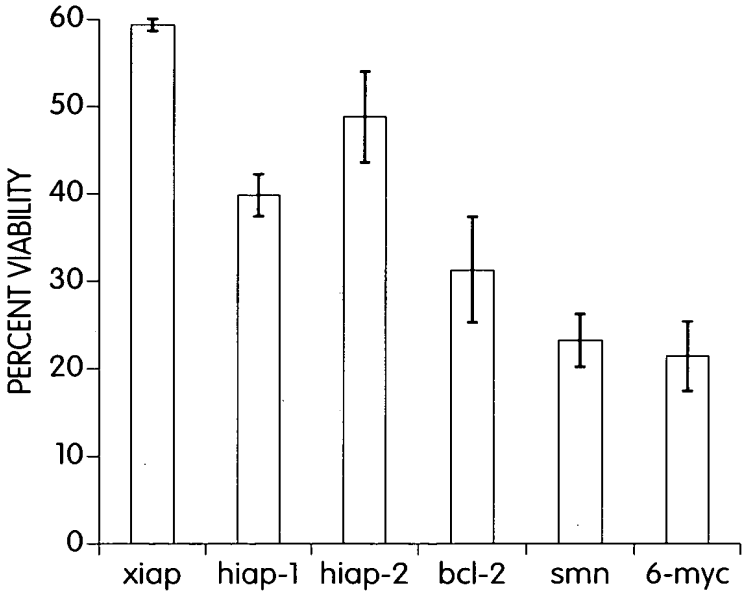


Fig. 14D

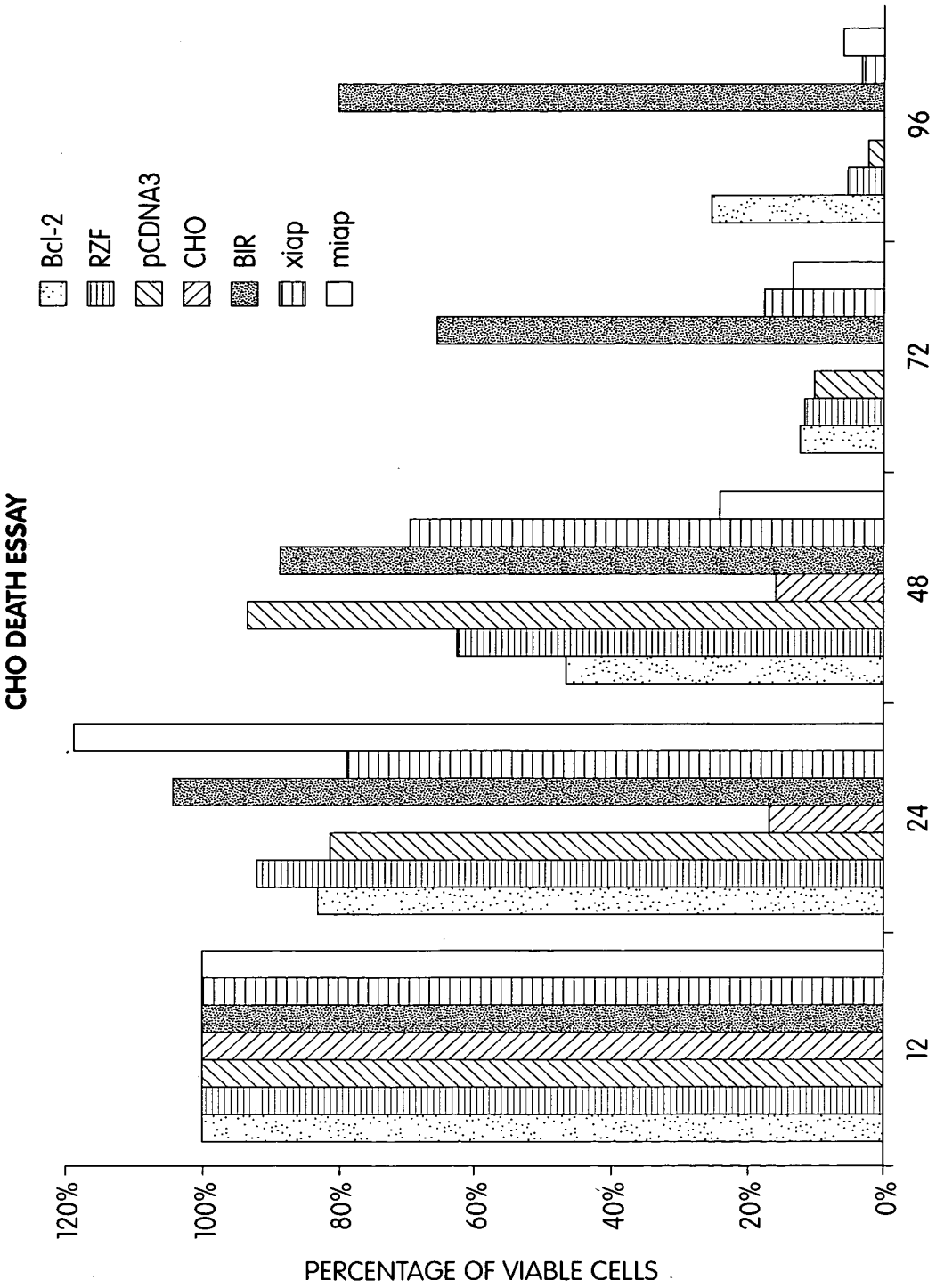
CHO DEATH ESSAY
Bcl-2
RZF
pCDNA3
CHO
BIR
xiap
miap
12
24
48
72
96
HOURS
120%
100%
80%
60%
40%
20%
0%
PERCENTAGE OF VIABLE CELLS

Fig. 15A

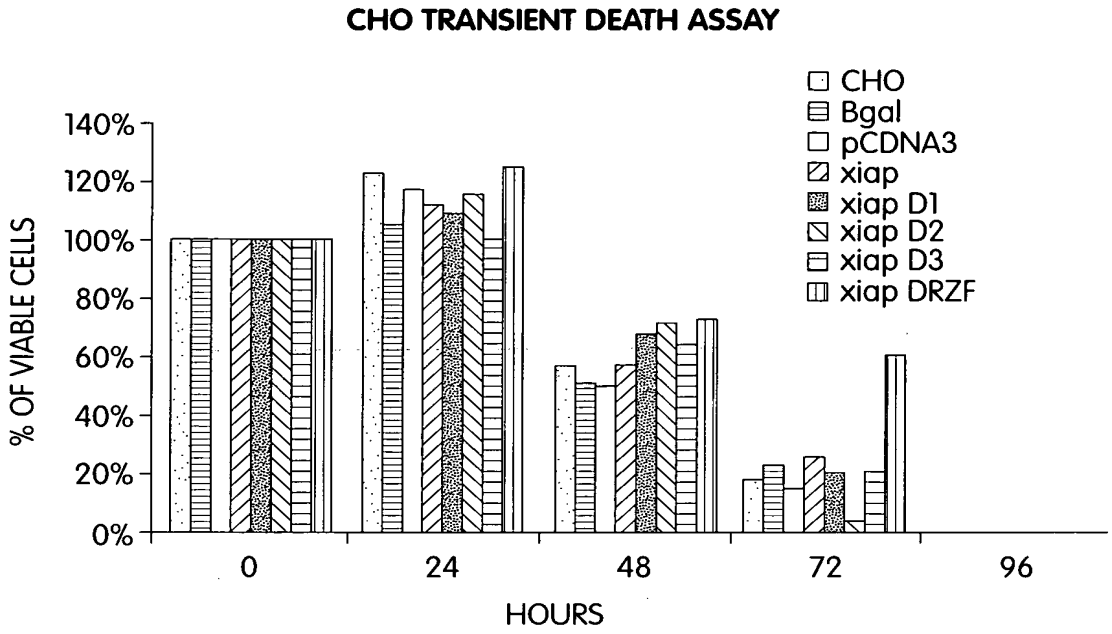
CHO TRANSIENT DEATH ASSAY
CHO
Bgal
pCDNA3
xiap
xiap D1
xiap D2
xiap D3
xiap DRZF
% OF VIABLE CELLS
140%
120%
100%
80%
60%
40%
20%
0%
0
24
48
72
96
HOURS

Fig. 15B

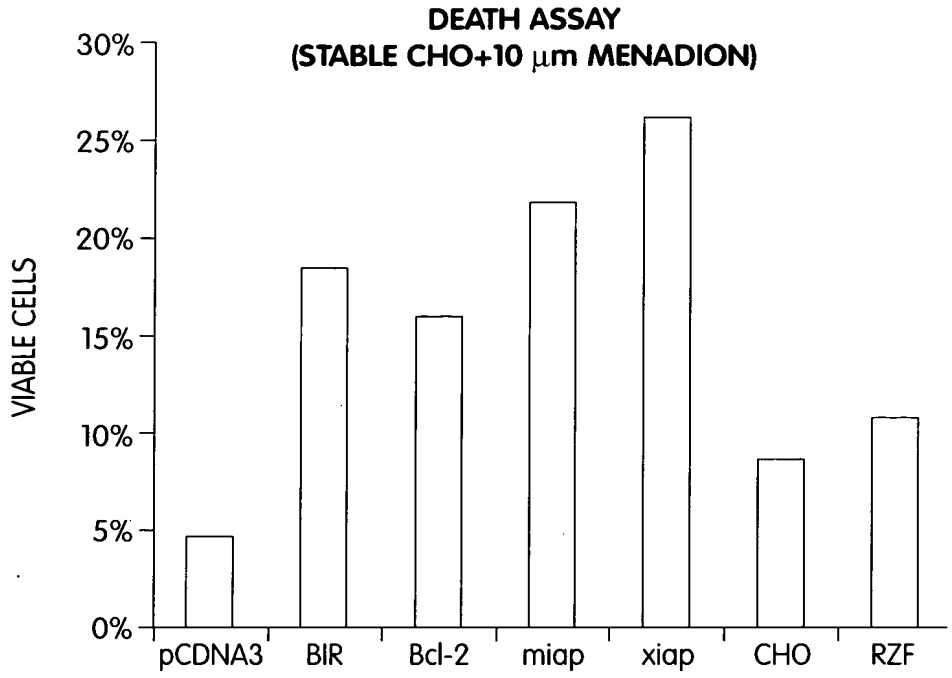


Fig. 16A

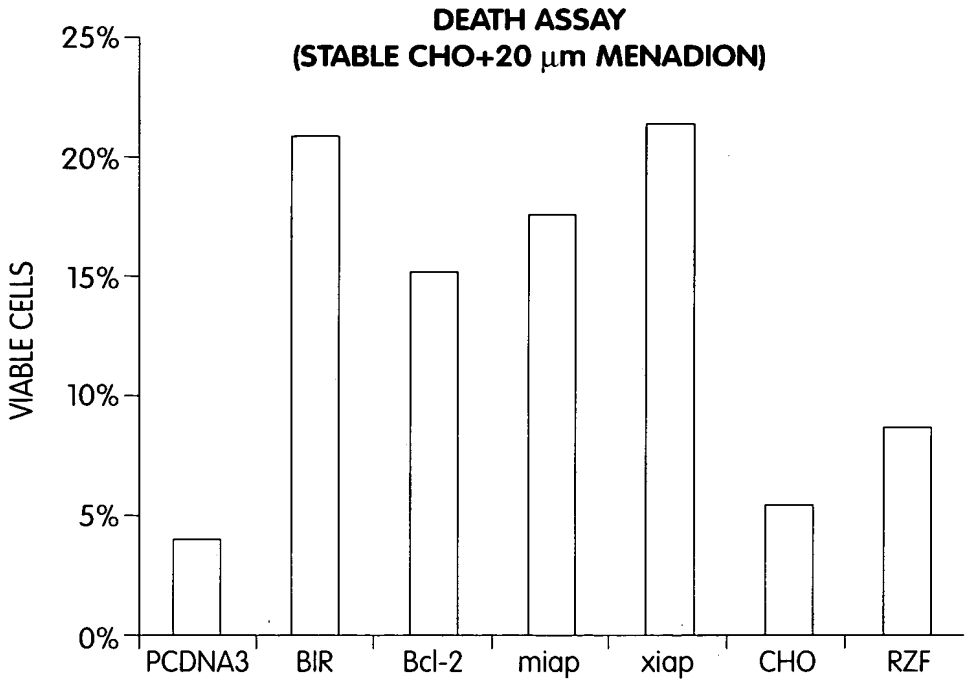


Fig. 16B

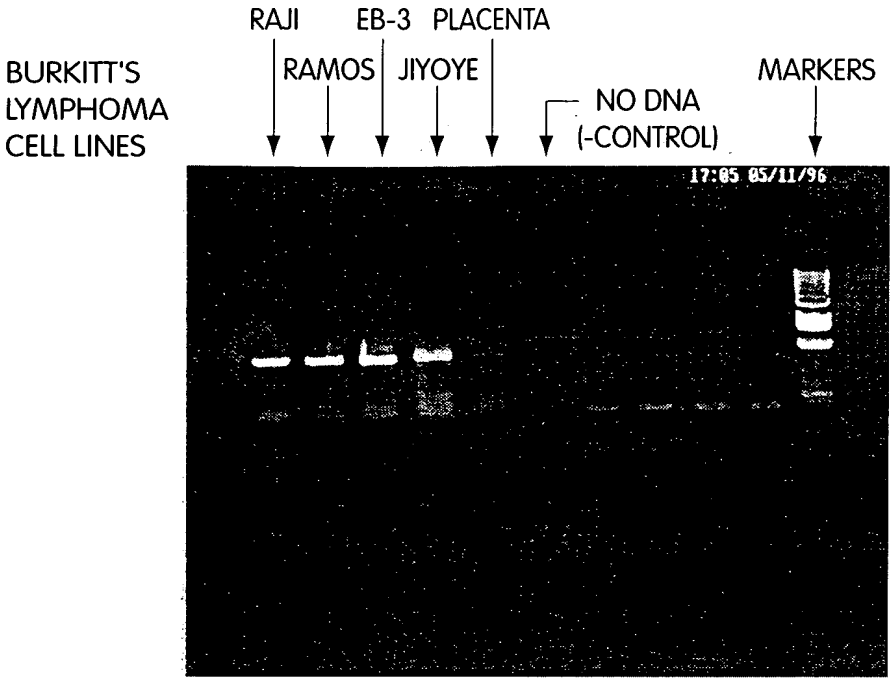
RAJI
EB-3
PLACENTA
BURKITT'S LYMPHOMA CELL LINES
RAMOS
JIYOYE
NO DNA (-CONTROL)
MARKERS
17:05 05/11/96

Fig. 17

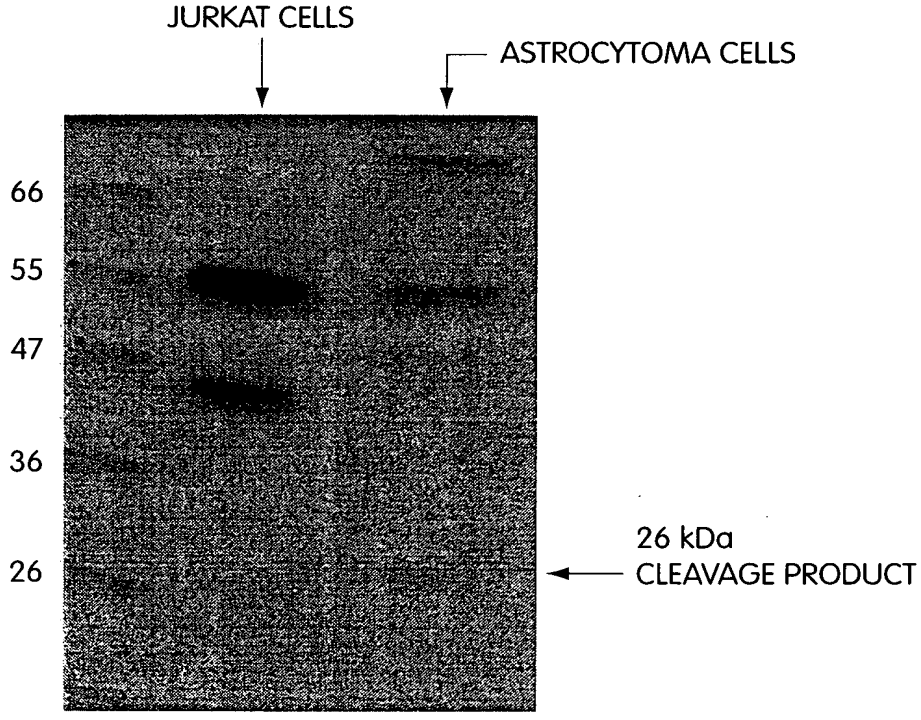
JURKAT CELLS
ASTROCYTOMA CELLS
66
55
47
36
26
26 kDa CLEAVAGE PRODUCT

Fig. 18

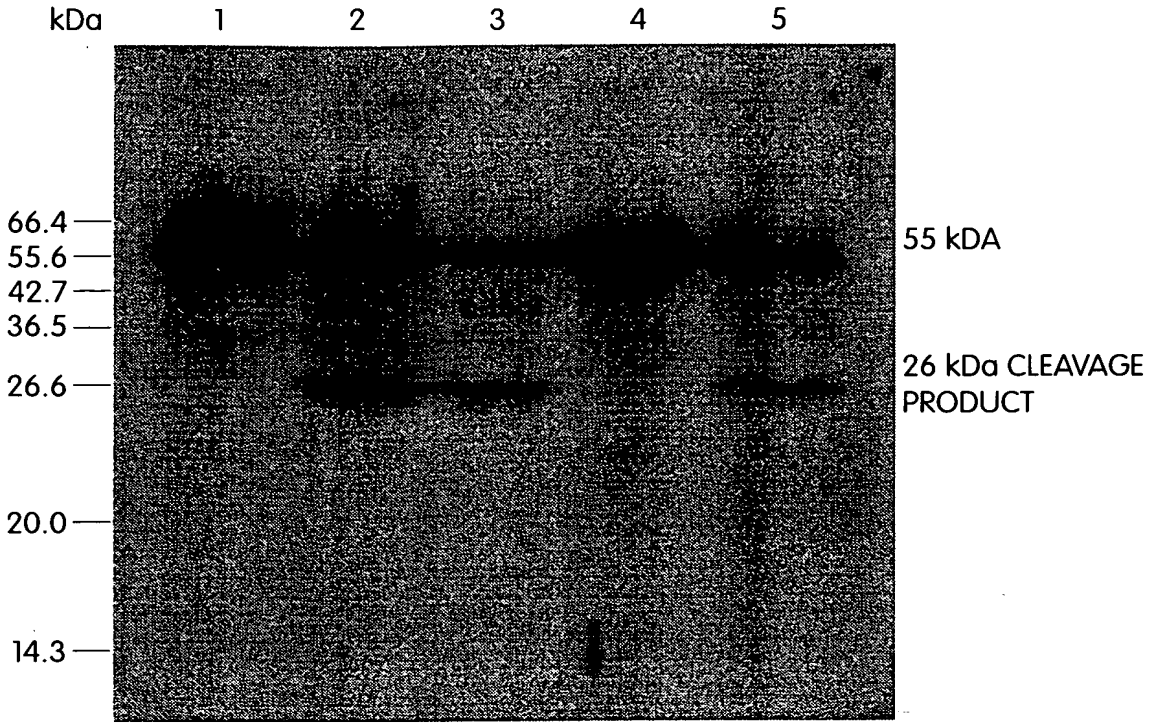
kDa
1
2
3
4
5
66.4
55.6
42.7
36.5
26.6
20.0
14.3
55 kDA
26 kDa CLEAVAGE PRODUCT

Fig. 19

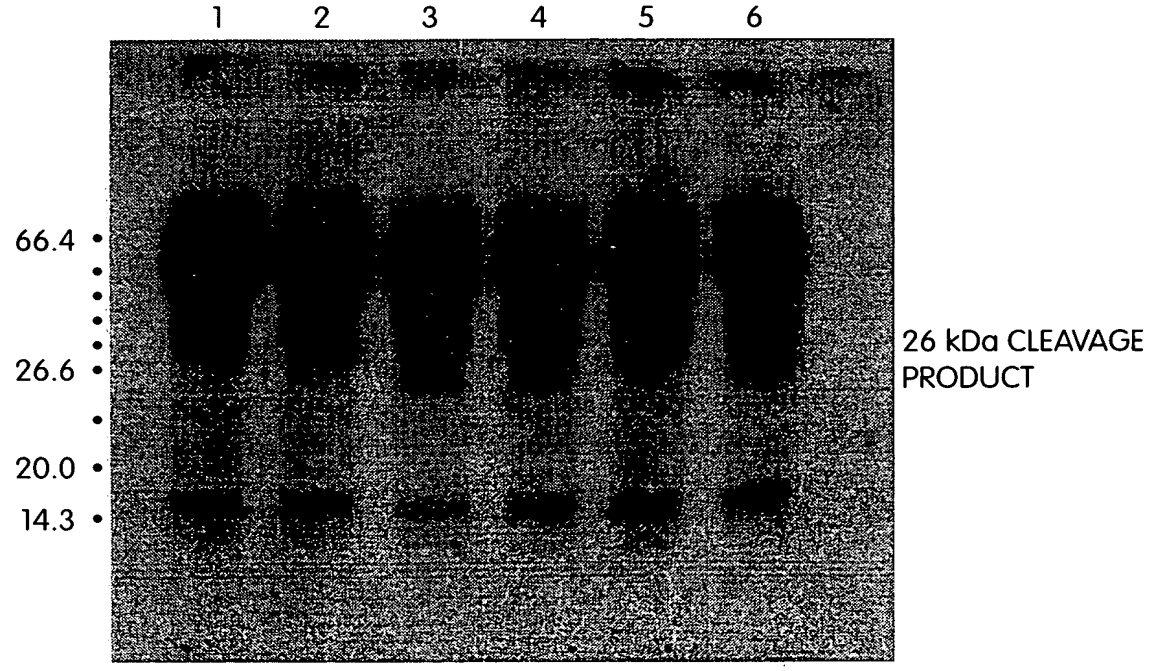
1
2
3
4
5
6
66.4
26.6
20.0
14.3
26 kDa CLEAVAGE PRODUCT

Fig. 20

HeLa

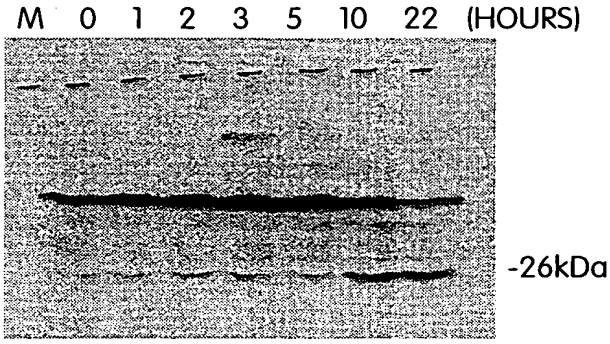


Fig. 21A

Jurkat

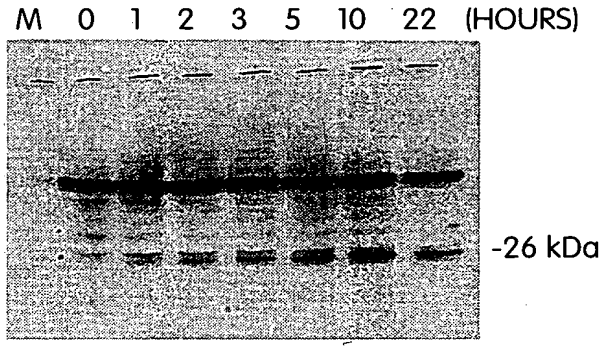


Fig. 21B

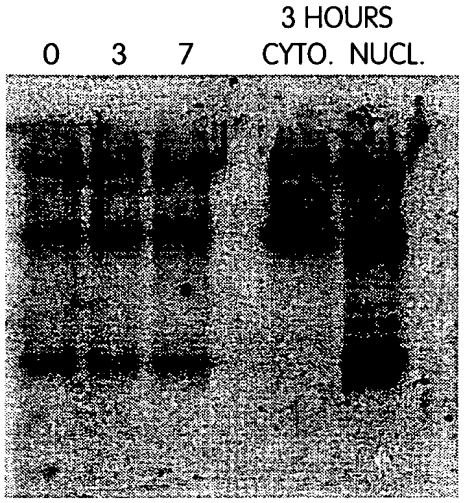


Fig. 22A

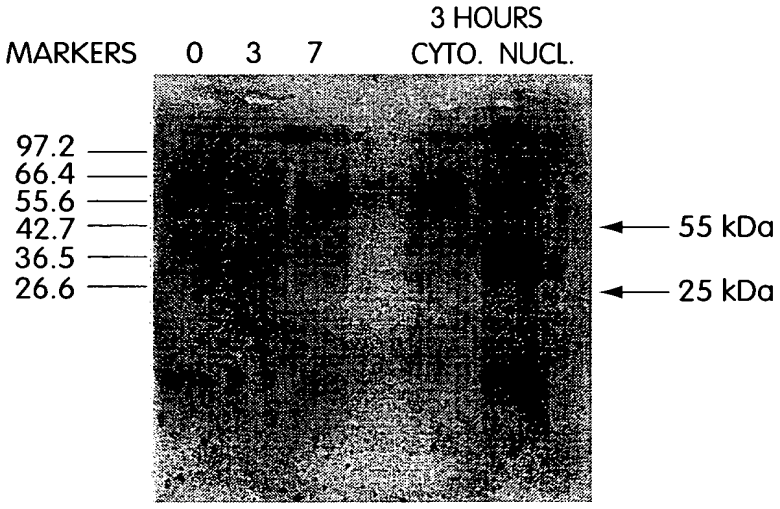


Fig. 22B

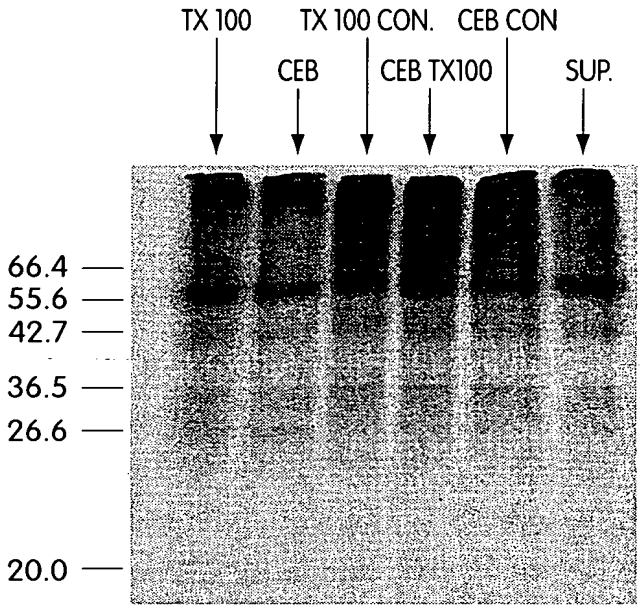
TX 100
TX 100 CON.
CEB CON
CEB
CEB TX100
SUP.
66.4
55.6
42.7
36.5
26.6
20.0

Fig. 23

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